

human MRPQGPAAAPQRLRGL--LLLLLLQLPAPSSASEIPKQKQKQALRQREVVDLYNGMCLQGPAGVPGROGSPGANGIPGTPGIPGRDGFKEGKECLRESF
 mouse MRPQGRAAPPQLLGLFLVLLLLQLSAPSSASENPKVQKALIRQREVVDLYNGMCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKEGKECLRESF
 rice_fish MTPLSRLLILLCLALPLHGQE--KGRSRGYRKDPDADKF--GSLQGPAGTPGRDGNPANGIPGTPGIPGRDGLKGEKGEVCVSEVF
 zebra_fish MGTKLTLQLLICFWISLPCVTKAKERIPRQ-RDAEFTDKYQA-CVQGVPGVQGRDGNPANGIPGTPGIPGRDGLKGEKGEVCVSEVF
 chicken RPREVLEAYNGVCLQGPSGVPGRDGNPANGIPGTPGIPGRDGPKEGKECLRESI
 Consensusll.....p.....k.....r.r#v...yng.ClQGp.GvpGRDGNPG.NGIPGTPGIPGRDG.KKEGKECLresf
 101 110 120 130 140 150 160 170 180 190 200
 human EESWTPNYKQCSWSSLYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMNSTINIHRTSSVE
 mouse EESWTPNYKQCSWSSLYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPELNSTINIHRTSSVE
 rice_fish EEPWKPNYKQCAWNSLYGIDLGKIAECTFTKLRSALRVLFSGSLRLKCKEACCQRWYFTFDGAECTGPLPVESIIYLNQGSPELNSTINIHRTSSVE
 zebra_fish EEPWKPNFKQCAWNSLYGIDLGKIAECTFTKQSDSALRVLFSGSLRLKCKTACCQRWYFTFNGAECTGPLPIESIVYLDQGSPELNSTINIHRTSTVE
 chicken EESWTPNFKQCSWNSLYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRSACCQRWYFTFNGAECAGPLPIEAIYYLDQGSPELNSTINIHRTSSVE
 Consensus EESwtPN%KQCSwssLYGIDLGKIA#CTFTKnRS#SALRVLFsGSLRLKCr.ACCQRWYFTF#GAEC.GPLP!Eai!YL#QGSPE\$NSTINIHRTSSVE

FIG. 1

human GLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNVSRIIEELPK
 mouse GLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNVSRIIEELPK
 rice_fish GLCEGIGAGLVDVALWVGTCDYPRGDASTGWNVSRIIEELPK
 zebra_fish GLCEGIHAGLVDVGIWVGTCDYPRGDASTGWNVSRIIEELPK
 chicken GLCEGINAGLVDIAIWVGTCSDYPRGDASTGWNVSRIIEELPK
 Consensus GLCEGI.AGLVD!aiWVGTCSDYPRGDASTGWNVSRIIEELPK

10 20 30 40 50
 MRPQGPAAAPQRLRGLLLLLLLQLPAPSSASEIPKQKQKQALRQREVVDLYNG
 60 70 80 90 100
 MCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKEGKECLRESFEESWTPNY
 110 120 130 140 150
 KQCSWSSLYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRWYF
 160 170 180 190 200 210
 TFNGAECSGPLPIEAIYYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVA
 220 230 240
 IWVGTCSDYPRGDASTGWNVSRIIEELPK

FIG. 2

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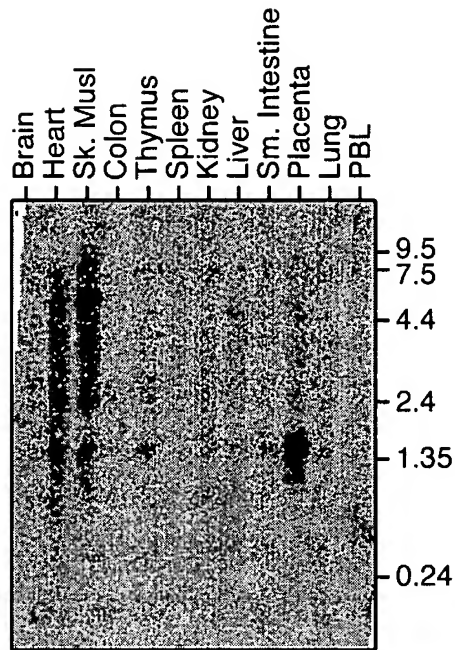


FIG. 3A

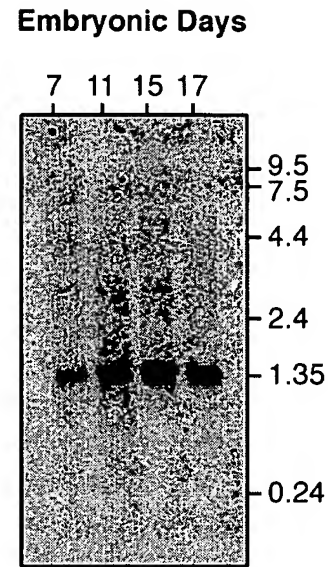


FIG. 3B

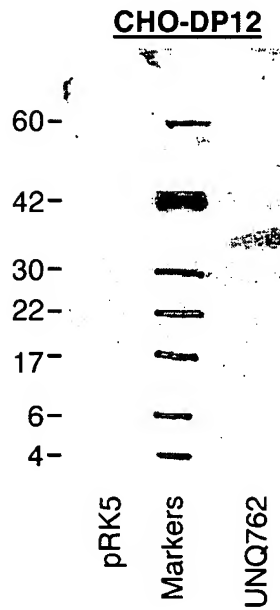


FIG. 4A

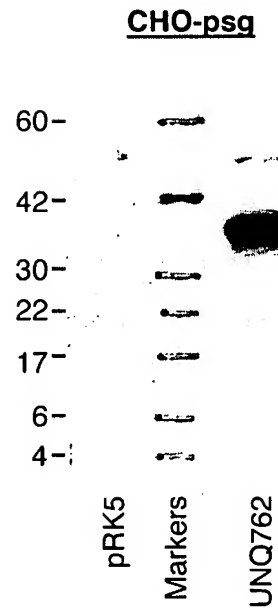


FIG. 4B



FIG. 5A

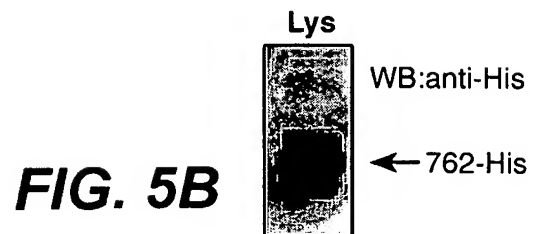


FIG. 5B

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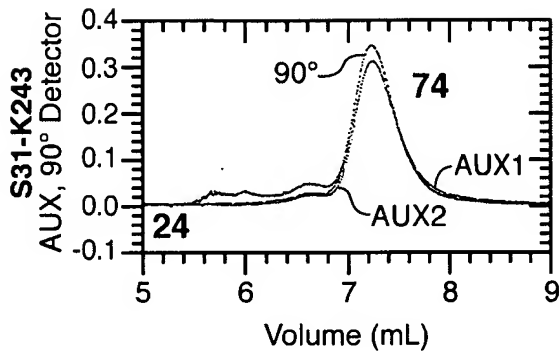


FIG. 6A

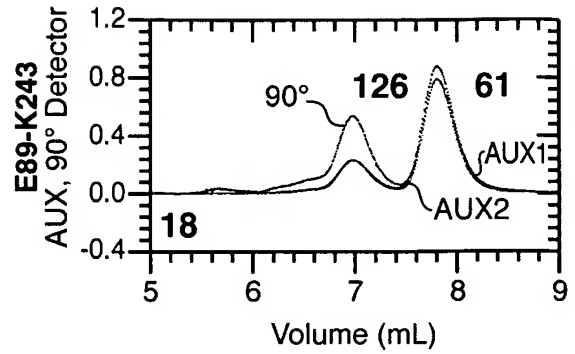


FIG. 6B

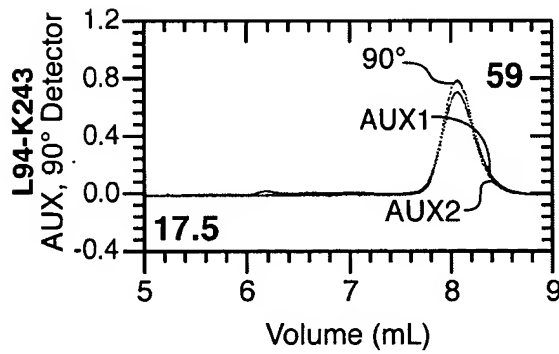


FIG. 6C

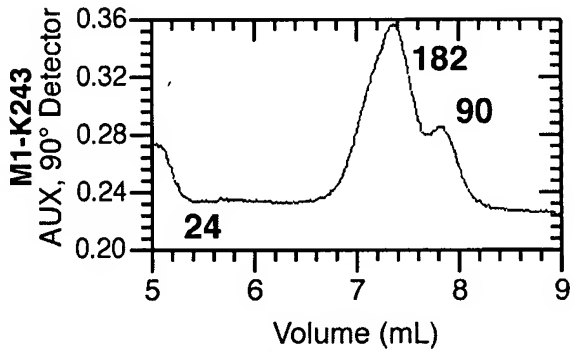


FIG. 7A

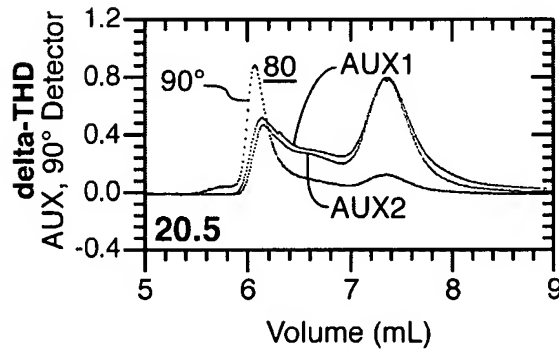


FIG. 7B

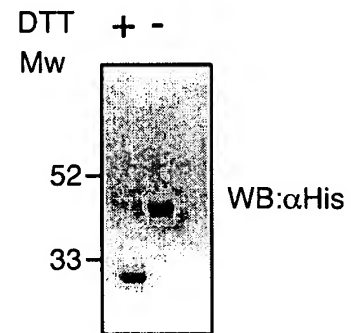


FIG. 7C

FIG. 8A

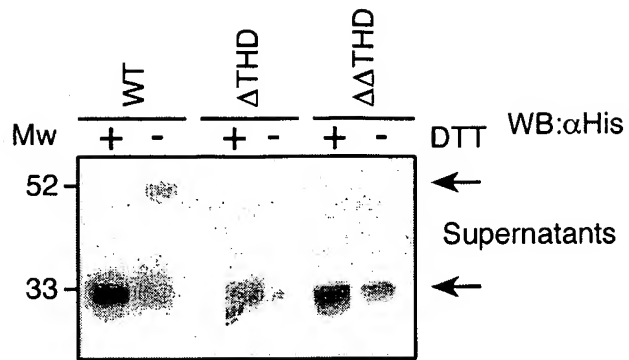


FIG. 8B

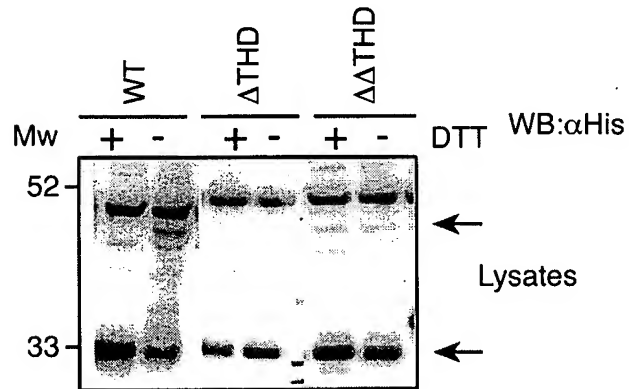


FIG. 9A

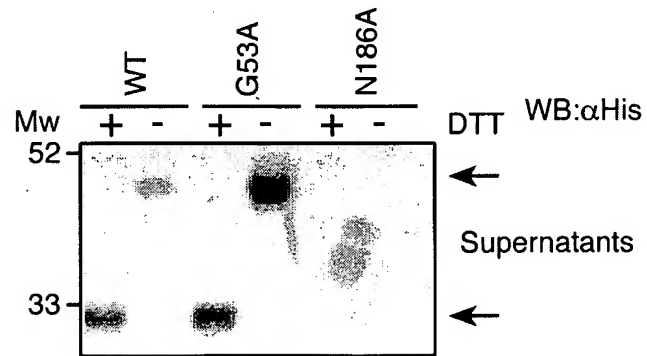


FIG. 9B

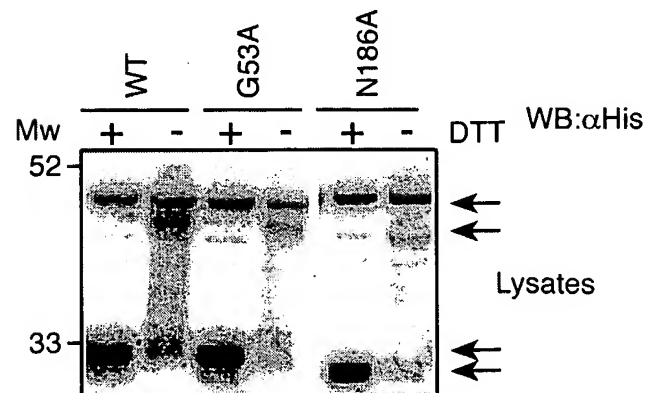
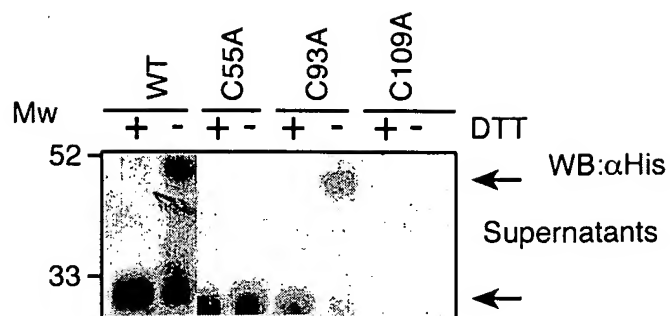
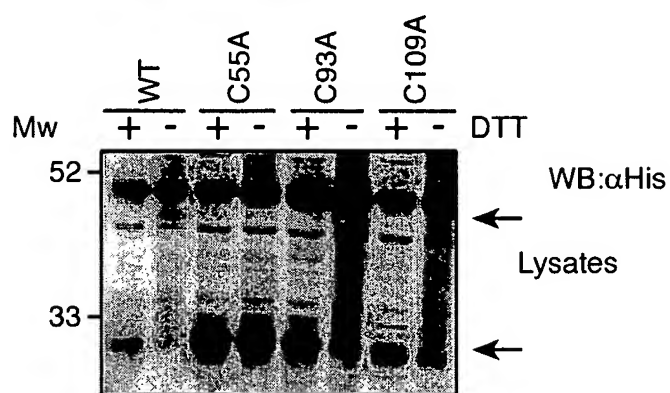
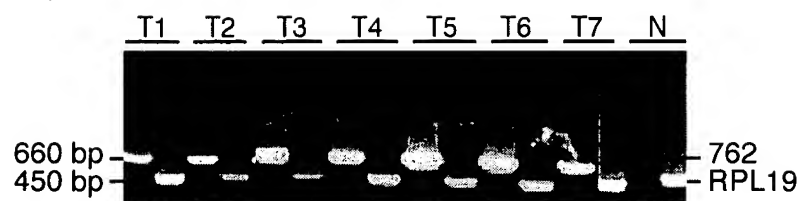
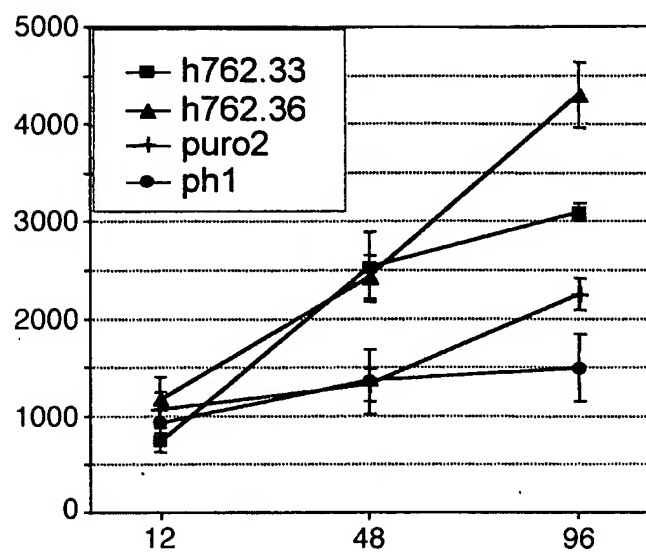
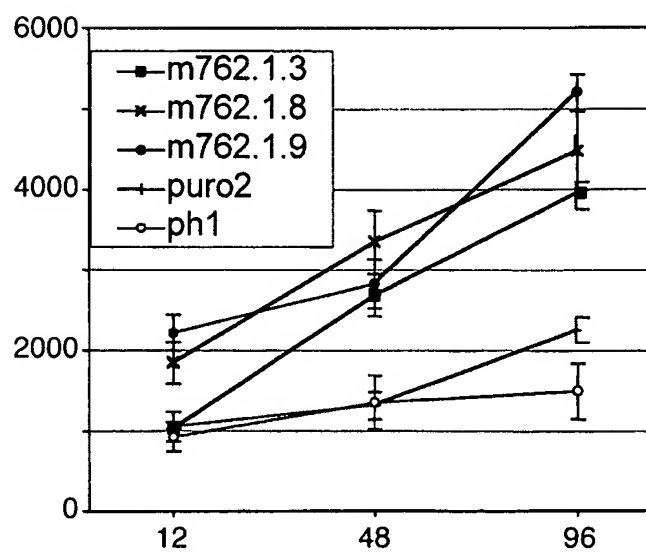


FIG. 10A**FIG. 10B****FIG. 11**

**FIG. 12A****FIG. 12B**

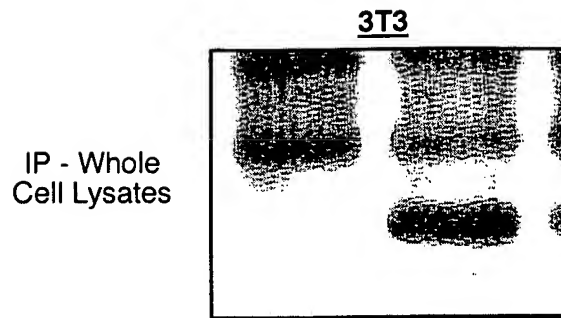


FIG. 13A

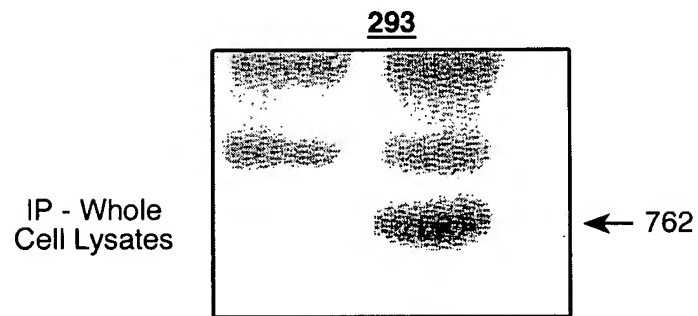


FIG. 13B

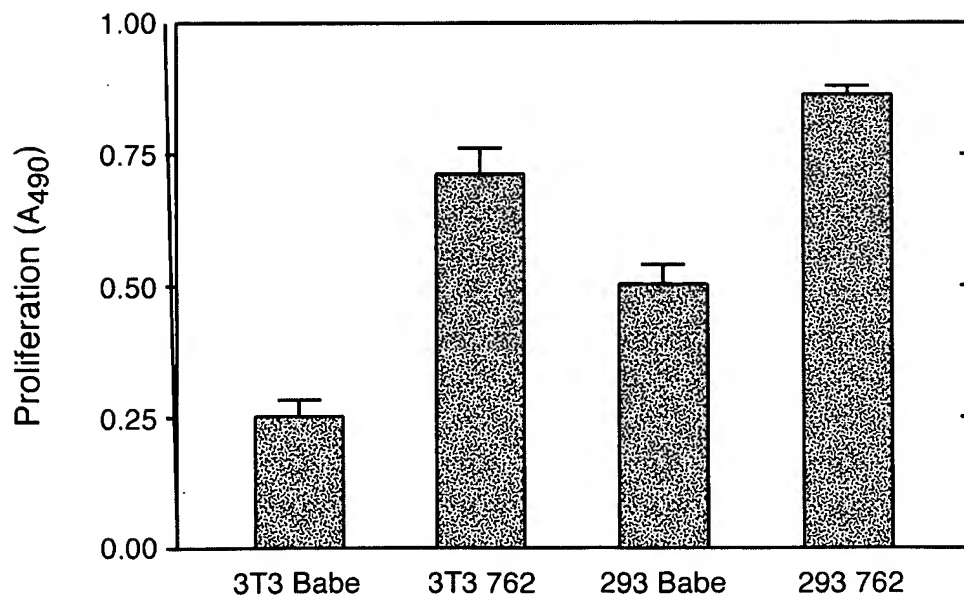
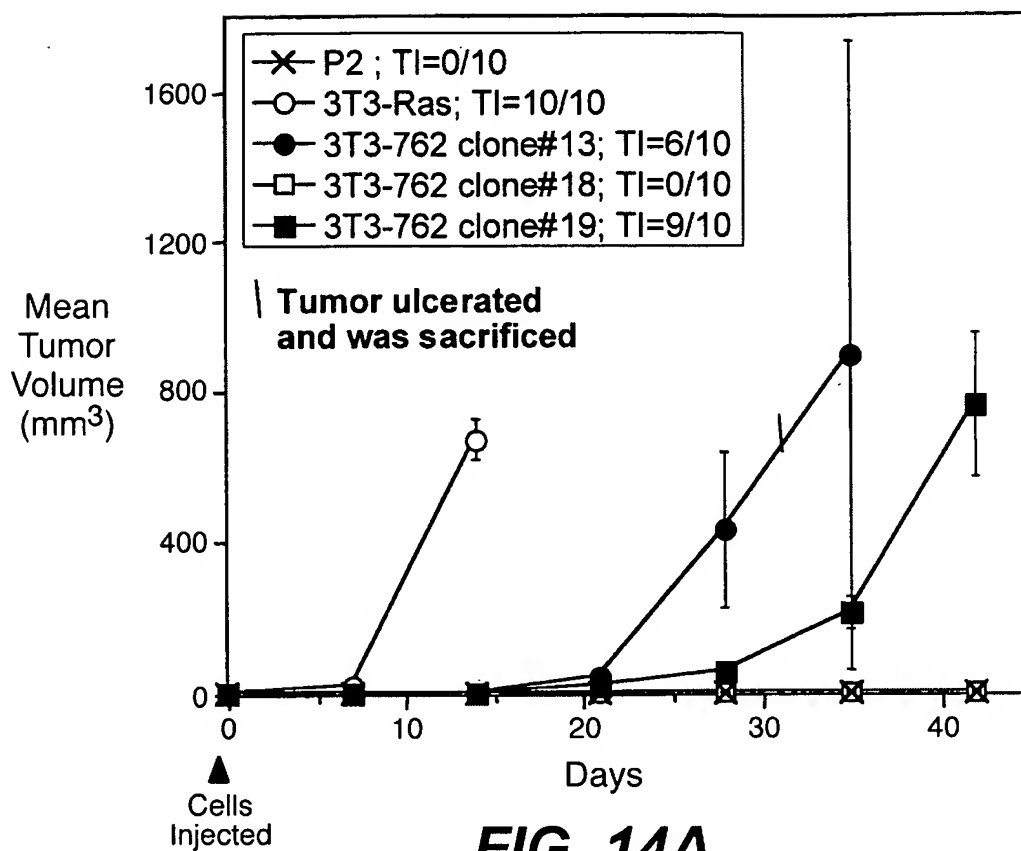
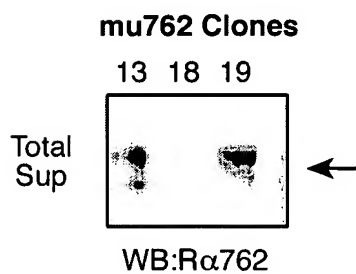
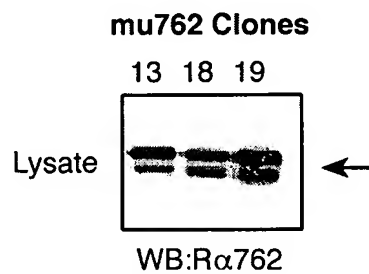
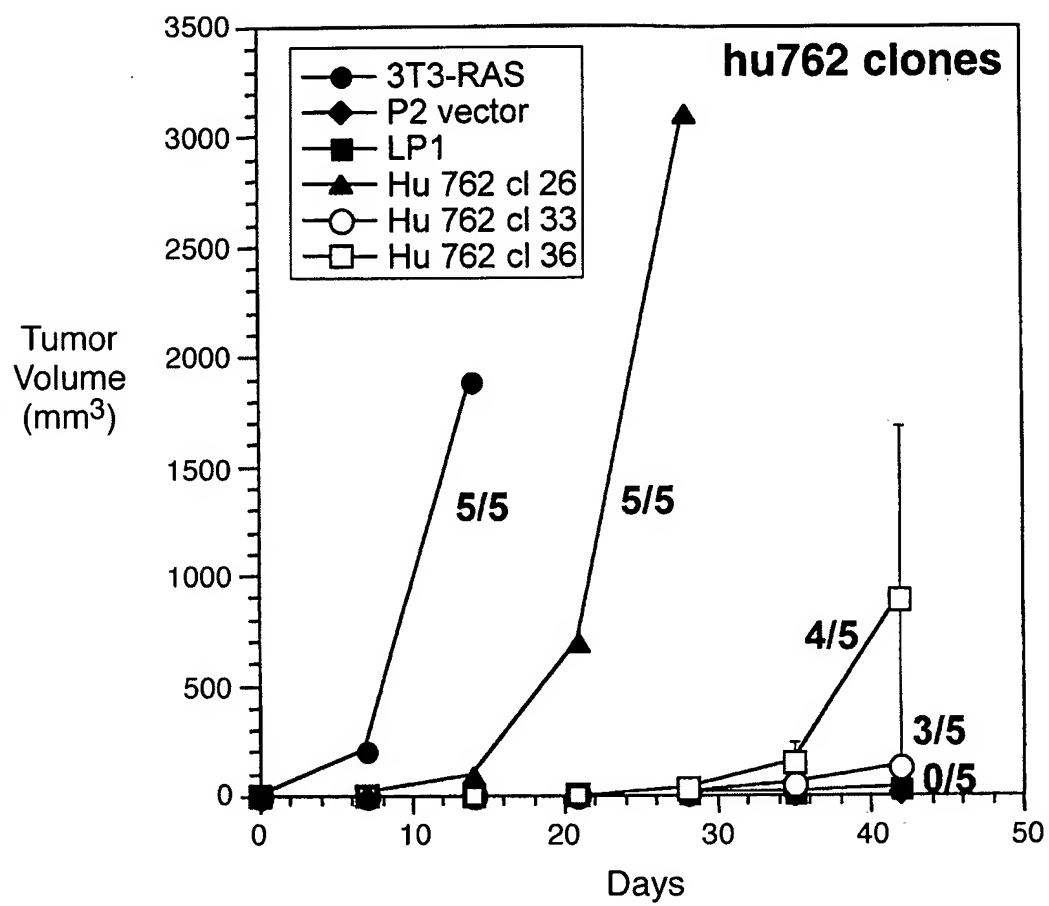


FIG. 13C

**FIG. 14A****FIG. 14B****FIG. 14C**

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**FIG. 15**

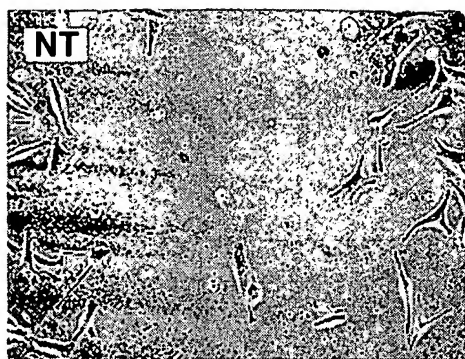


FIG. 16A



FIG. 16C



FIG. 16B

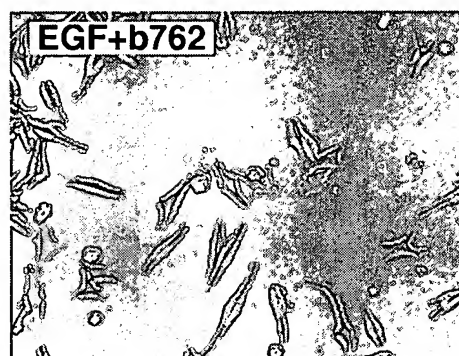


FIG. 16D

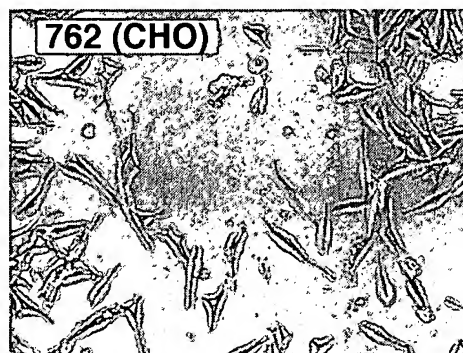


FIG. 16E

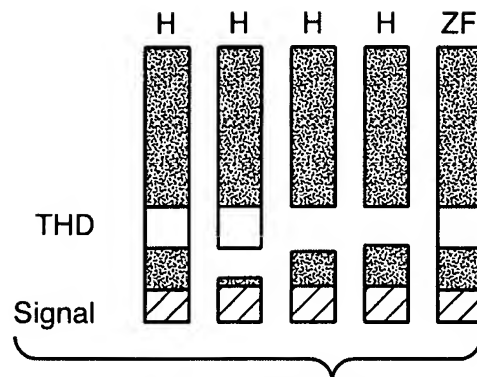


FIG. 17A

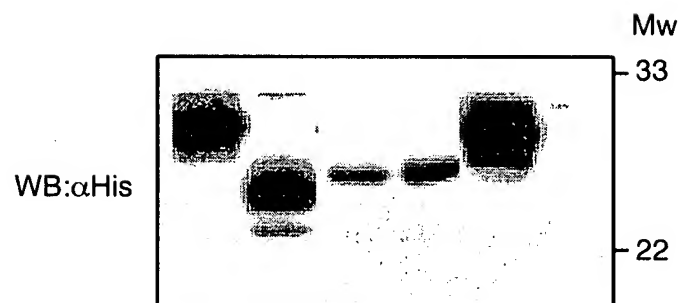


FIG. 17B

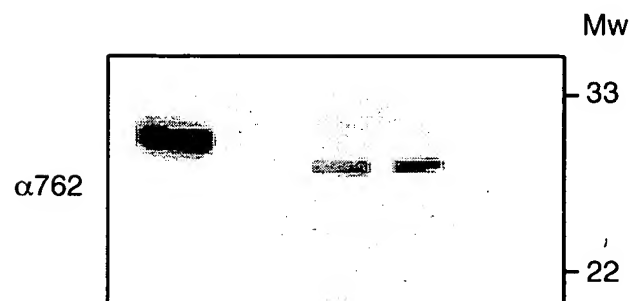


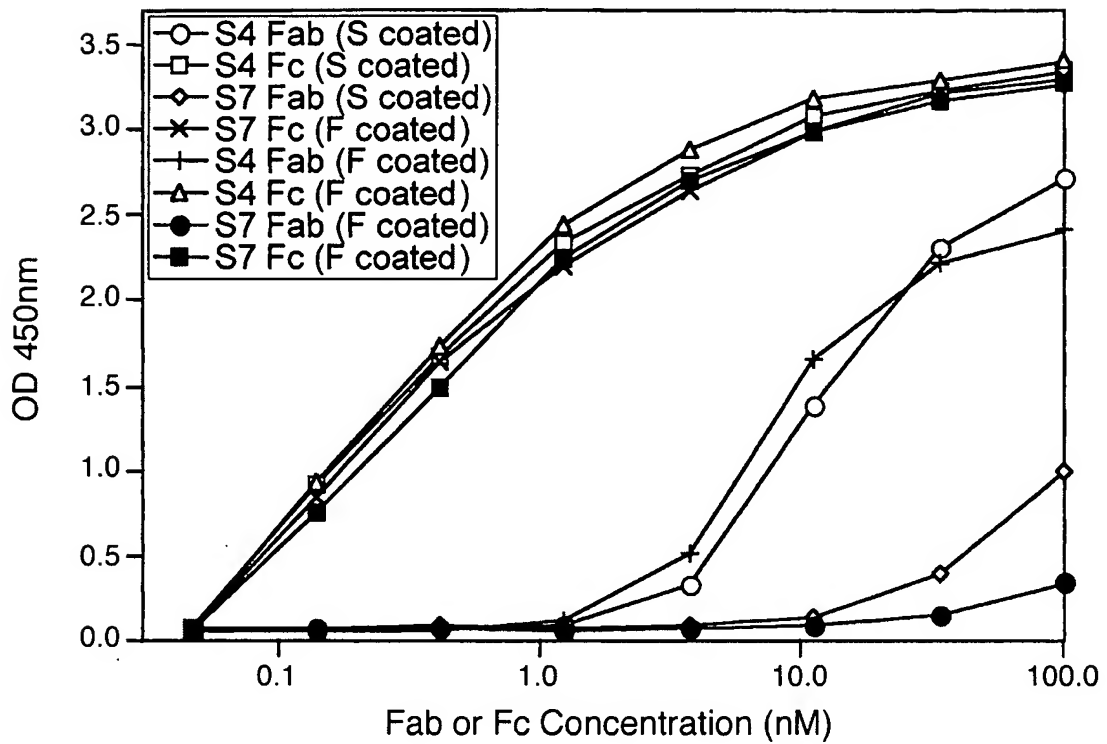
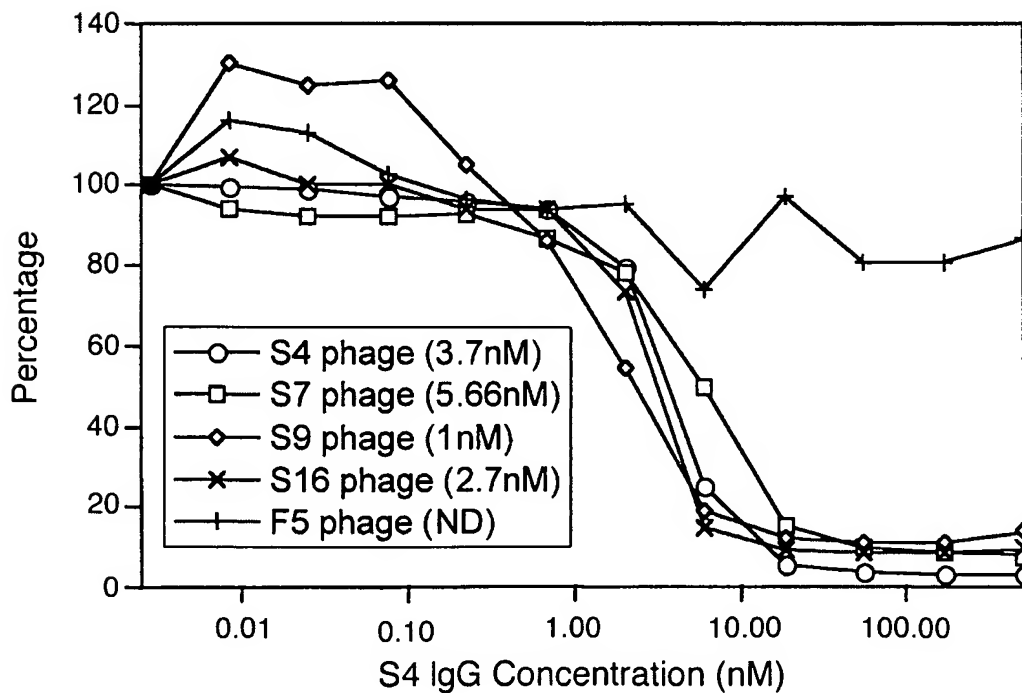
FIG. 17C

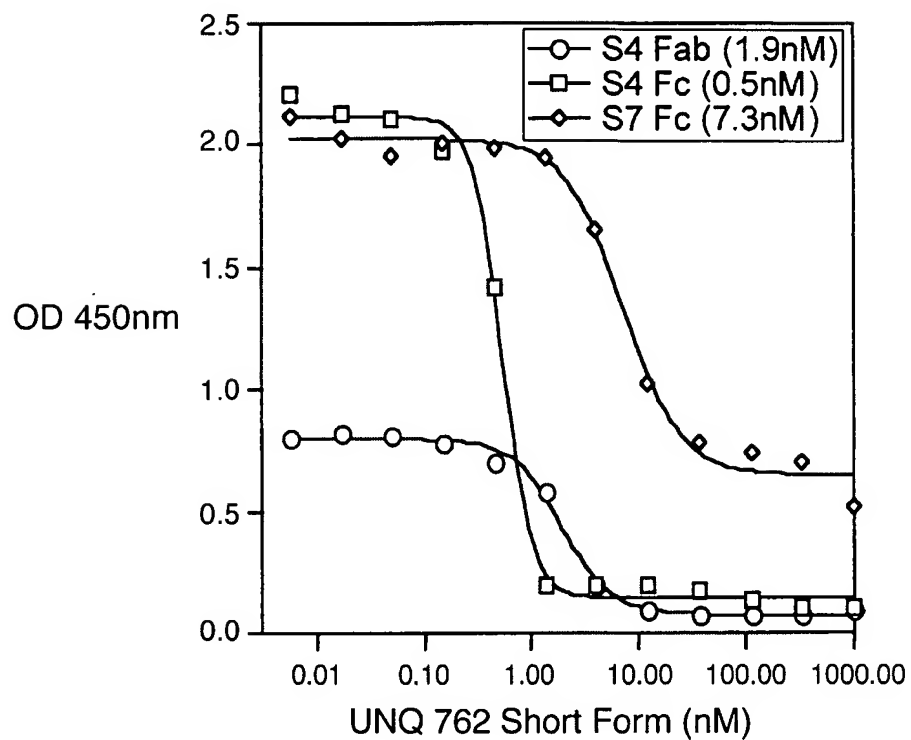
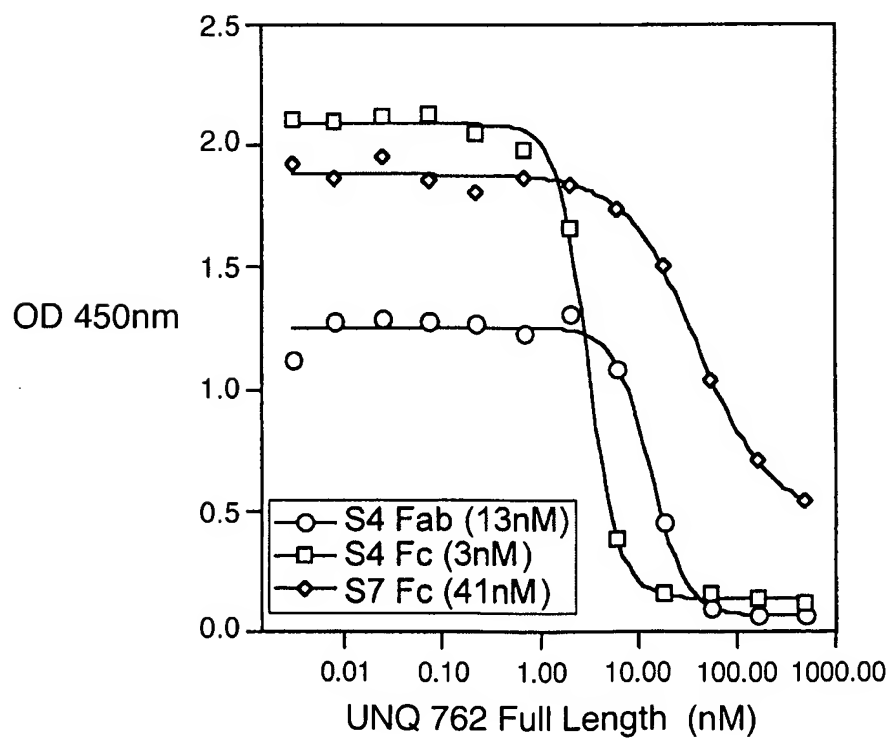
HI						H2											H3											Name			
28	29	30	31	32	33	49	50	51	52	52a	53	54	55	56	57	58	92	93	94	95	96	97	98	99	100	100a	100b		100c	101	102
T	I	S	G	S	D	G	R	I	S	P	Y	G	G	N	T	N	C	A	R	V	G	G	L	K	L	L	-	F	D	Y	S7
T	I	T	N	S	D	A	T	I	Y	P	Y	G	G	Y	T	Y	C	A	R	G	G	G	M	D	G	Y	V	M	D	Y	S16
T	I	N	N	Y	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	F5
T	I	N	N	Y	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	F6
T	I	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	S4
T	I	S	N	Y	G	G	R	I	S	P	S	N	G	S	T	Y	C	A	K	C	S	V	R	-	-	-	-	F	A	Y	S9
T	I	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	F13
T	I	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	F47

FIG. 18

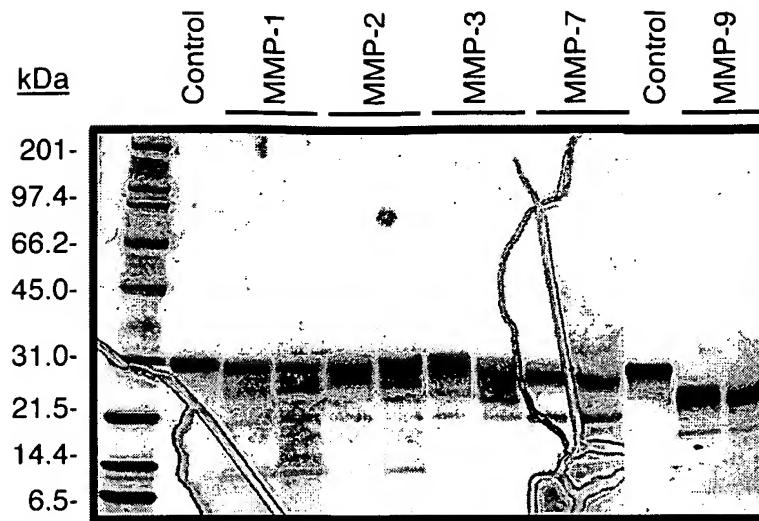
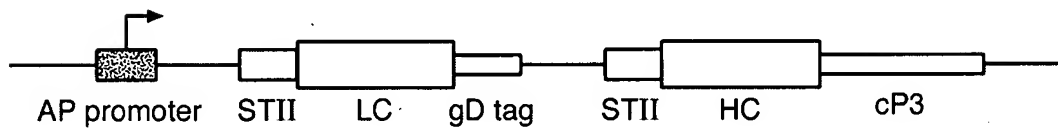
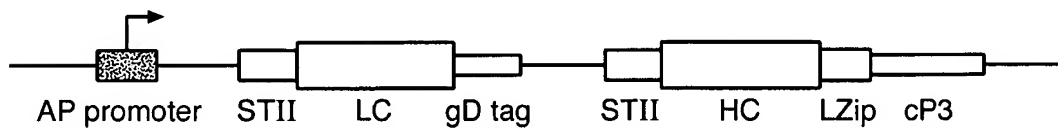
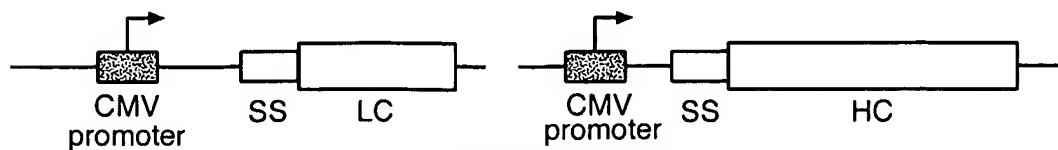
	Phage		Fab		IgG	
S4	762 S/S	762 F/F	762 S/S	762 F/S	762 S/S	762 F/F
	3nM	0.9nM	3.6nM (1.9nM)	32nM	0.5nM	3.1nM
S7	762 S/S	762 F/F	762 S/S	762 F/S	762 S/S	762 F/F
	35nM	2.7nM	113nM	57nM	7.3nM	41nM

FIG. 21

**FIG. 19****FIG. 22**

**FIG. 20A****FIG. 20B**

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**FIG. 23****FIG. 24A****FIG. 24B****FIG. 24C****FIG. 24D**

```

1 GAATCAACT TCTCCATACT TTGGATAGG AATACAGAC ATGAAAAATC TCAFTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAGA AGAGTCGAAT
  CTTAAGTTGA ACAGGTATGA AACCTATTCC TTTATGCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCTCA CTGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
  CTGACACAC CCGTCCATCT TCGAAACCTC TAATAGGAGT GACGTACGA AGCTTATAC CCGTTTTTAC TGGTTGTCG CAACTAATA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA CGACGATACG GAGTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
  CCGCGGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCACA GCTGTCTATA AGTTGTCAG GCGGAGACTT ATACGCTCTT TGTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
  TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATGTA GAGGTTGAGG TGATTTTATG AAAAGAATA TCGCATTTCT TCTTGCATCT ATGTTTCGTTT TTTCTATTGC TACAAATGCC
  AGTGCATTTT TCCCATACAT CTCCAATCC ACTAAATAC TTTTCTTAT AGCGTAAAGA AGAAGCTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG
  1 M K K N I A F L L A S M F V F S I A T N A
    ^start of still signal sequence
    ^met

501 TATCAGATA TCCAGATGAC CCAGTCCCCG AGCTCCCTGT CCGCTCTGT GGGCGATAGG GTACCCATCA CCTGCCGTGC CAGTCAGGAT GTGTCCACTG
  ATACGTCTAT AGGTCTACTG GGTACAGGGC TCGAGGGACA GCGGAGACA CCCGTATCC CAGTGGTAGT GGACGGCAGC GTCAGTCTTA CACAGGTGAC
  22 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T A
    ^start of light chain
    ^CDR-L1

601 CTCTAGCCTG GTATCAACAG AAACCAGGAA AAGCTCCGAA GCTTCTGATT TACTCGGCAT CCTTCTCTTA CTCTGGAGTC CCTTCTCGCT TCTCTGGTAG
  GACATCGGAC CATAGTTGTC TTTGGTCTTT TTCGAGGCTT CGAAGACTAA ATGAGCGTA GGAAGGAGAT GAGACCTCAG GGAAGAGCGA AGAGACCATC
  56 V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S
    ^CDR-L2

701 CGGTCCGGG ACGGATTCA CTCTGACCAT CAGCAGTCTG CAGCCGAAG ACTTCGAAC TTATTACTGT CAGCAATCTT ATACTACTCC-TCCCACGTTT
  GCCAAGGCC TGCATAAGT GAGACTGGTA GTCGTCAGAC GTCGGCTTC TGAAGCTTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGTTGCAAG
  89 G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F
    ^CDR-L3

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FIG._25A

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801 GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGGTG CACCACTGTG CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCTCTG
    CCTGTCCCAT GGTTCACCT CTAGTTTGCT TGACACCGAC GTGGTAGACA GAAGTAGAAG GCGGGTAGAC TACTCGTCAA CTTTAGACCT TGACGGAGAC
122 G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V

901 TTGTGTGCT GGTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACAGTGG AAGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTCACAGA
    AACACACGGA CGACTTATTG AAGATAGGGT CTCTCCGGTT TCATGTCACC TTCCACCTAT TCGGGGAGGT TAGCCCATTG AGGTCTCTCT CACAGTGTCT
156 V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E

1001 GCAGGACAGC AAGACAGCA CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAAGCAGA CTACAGAGAA CACAAAGTCT AGCCTGCGA AGTCACCCAT
    CGTCTGTGCG TTCCTGTGCT GGATGTCGGA GTCGTGCTGG GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TCGGGACGCT TCAGTGGGTA
189 Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H

1101 CAGGGCCTGA GCTGCCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTCCGGCGT AAGGACCTGG
    GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCCC CTCTCACACC ACGGTGAGG CCATACCGAC TAGGCTTGGC AAAGCGGCA TTCCTGGACC
222 Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L A
    ^end of light chain, start of gp tag

1201 CATAACTCGA GGCTGATCCT CTACGCCGGA CGCATCGTGG CCCTAGTACG CAAGTTCACG TAAAAGGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA
    GTATTGAGCT CCGACTAGGA GATGCGGCCCT GCGTAGCACC GGGATCATGC GTTCAAGTGC ATTTTTCCTCA TTGATCTCCA ACTCCACTAA AATACITTTT
256 O
-23

1301 GAATATCGCA TTTCTTCTTG CATCTATGTT CGTTTTTTCT ATTGCTACAA ACGCGTACGC TGAGGTTTCAG CTGGTGGAGT CTGGCGGTGG CCTGGTGCAG
    CTTATAGCGT AAAGAAGAAC GTAGATACAA GCAAAAAAGA TAACGATGTT TGCGCATGCG ACTCCAAGTC GACCACCTCA GACCGCCACC GGACCCAGTC
-20 N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q
    ^start of heavy chain

1401 CCAGGGGGCT CACTCCGTTT GTCTGTGCA GCTTCTGGGT TCAACATTAAG AGACACCTAT ATACACTGGG TCGGTCAGGC CCCGGGTAG GGCCTGGGAT
    GGTCCCCCGA GTGAGGCAAA CAGGACACGT CGAAGACCGA AGTTGTAAAT TCTGTGGATA TATGTGACCC ACGCAGTCCG GGGCCCATTC CCGGACCTTA
14 P G G S L R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E W
    ^CDR-H1

```

M K K
^start of stII

FIG..25B

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```

1501 GGGTTGCAAG GATTATATCTT ACGAATGGTT ATACTAGATA TGCAGATAGC GTCAAGGGCC GTTTCACATAT AAGCGCAGAC ACATCCAAAA ACACAGCCTA
      CCCAACGTTT CTAAATAGGA TGCTTACCAA TATGATCTAT ACGGTATATCG CAGTCCCGG CAAAGTGATA TTGCGGTCTG TGTAGTTTTT TGTGTGGGAT
48  V A R I Y P T N G Y T R Y A D S V K G R F T I S A D T S K N T A Y
      ^CDR-H2

1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATTATTGTA GCGCTGGGG AGGGACGGC TTCTATGCTA TGGACTACTG GGTCAAGGA
      GGATGTTTAC TTGTGGAATF CTCGACTCCT GTGACGGCAG ATATAACAT CGGCGACCCC TCCCCTGCCG AAGATACGAT ACCTGATGAC CCCAGTTCCT
81  L Q M N S L R A E D T A V Y Y C S R W G G D G F Y A M D Y W G Q G
      ^CDR-H3

1701 ACACTAGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT CCGTCTTCCC CTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACACGG GCCCTGGGCT
      TGTGATCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA GCCAGAGGG GGACCGTGGG AGGAGTTCT CGTGGAGACC CCCGTGTGCG CGGGACCCGA
114 T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C

1801 GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAATCTA GGGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC
      CGGACCAGTT CCTGATGAAG GGGCTTGGCC ACTGCCACAG CACCTTGAGT CCGCGGGACT GGTGCGCGCA CGTGTGGAAG GGCCGACAGG ATGTCAGAG
148 L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S

1901 AGGACTCTAC TCCCTCAGCA GCGTGTGTGAC GGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCGAG CAACACCAAG
      TCCTGAGATG AGGGAGTCGT CGCACCACTG GCACGGGAGG TCCTGCAACC CCGTGGTCTG GATGTAGACG TTGCACCTAG TGTTCGGGTC GTTGTGGTTC
181 G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K

2001 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAACTC ACCTCAGTGG CCGTGGCTCT GTTCCGGTG ATTTTGATTA TGAAAAGATG GCAAACGCTA
      CAGCTGTTCT TTCAACTCGG GTTTAGAAC A CTGTTTGTAG TGGAGTCACC GCCACCGAGA CCAAGGCCAC TAAAACTAAT ACTTTTCTAC CGTTTGGGAT
214 V D K K V E P K S C D K T H L S G G S G S G D F D Y E K M A N A N

      ^end of heavy chain
      ^start of gene III coat protein (267-end)

2101 ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGGCT ACAGTCTGAC GCTAAAGGA AACTTGATTC TGTGCTACT GATTACGGTG CTGCTATCGA
      TATTCCCCCG ATACTGGCTT TTACGGCTAC TTTTGGCGGA TGTACAGACTG CGATTCCGT TTGAACTAAG ACAGCGATGA CTAATGCCAC GACGATAGCT
248 K G A M T E N A D E N A L Q S D A K G K L D S V A T D Y G A A I D

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FIG._25C

2201 TGGTTTCATT GGTGACGTTT CCGGCCCTGC TAAATGGTAAT GGTGCTACTG GTGATTTTGC TGGCTCTPAAT TCCCAATAGG CTCAACTCGG TGACGGTGAT
 ACCAAAGTAA CCACTGCAAA GGCCGGAACG ATTACCATTA CCACGATGAC CACTAAACG ACCGAGATTA AGGTTTACC GAGTTACGCC ACTGCCACTA
 281 G F I G D V S G L A N G N G A T G D F A G S N S Q M A Q V G D G D
 2301 AATTCACCTT TAATGAATAA TTTCCTGCAA TATTACCTT CCTCCCTCA ATCGGTTGAA TGTGCCCCCTT TTGTCTTTAG CGCTGGTAAA CCATATGAAT
 TTAAGTGGAA ATTACTTATT AAAGGCAGTT ATAAATGGAA GGAGGGAGT TAGCCAACTT ACAGCGGGA AACAGAAATC GCGACCATTT GGTATACTTA
 314 N S P L M N N F R Q Y L P S L P Q S V E C R P F V F S A G K P Y E F
 2401 TTTCATTTGA TTGTGACAAA ATAACTTAT TCCGTGGTGT CTTTGGGTTT CTTTATATG TTGCCACCTT TATGTAAGTA TTTTCTACGT TTGCTAACAT
 AAAGATAACT AACACTGTTT TATTTGAATA AGGCACCACA GAACGCAAA GAAATATATAC AACGGTGGAA ATACATACAT AAAAGATGCA AACGATTGTA
 348 S I D C D K I N L F R G V F A F L L Y V A T F M Y V F S T F A N I
 2501 ACTGCGTAAT AAGGAGTCTT AATCATGCCA GTTCTTTTGG CTAGCGCCGC CCTATACCTT GTCTGCCCTC CCGCGTTGG TCGGGTGCA TGGAGCCGGG
 TGACGCATTA TTCTCAGAA TTAGTACGGT CAAGAAAACC GATCGCGCG GATATGGAA CAGACGGAGG GCGCAACGC AGCGCACGT ACCTCGGCC
 381 L R N K E S O
 2601 CCACCTCGAC CTGAATGGAA GCCGGCGGCA CCTCGCTAAC GGATTCACCA CTCCAAGAAT TGGAGCCAAAT CAATTCTTGC GGAGAATGT GAATGCGCAA
 GGTGGAGCTG GACTTACCTT CGGCCGCCGT GGAGCGATTG CTTAAGTGGT GAGGTTCTTA ACCTCGGTTA GTTAAGAAAG CCTCTTGACA CTTACCGCTT
 2701 ACCAACCTT GGCAGAACAT ATCCATCGCG TCCGCCATCT CCAGCAGCG CACGCGGCG ATCTCGGGA GCGTTGGTGC CTGGCCACGG GTGCGCATGA
 TGGTTGGGA CCGTCTTGTA TAGGTAGCGC AGGCGTAGA GGTGTCGGC GTGCGCCCG TAGAGCCCGT CGCAACCCAG GACCGGTGCC CACGCGTACT
 2801 TCGTGCTCCT GTCGTTGAGG ACCCGGCTAG GCTGGCGGGG TTGCTTACT GGTAGCAGA ATGAATCACC GATACGCGAG CGAACCTGAA GCGACTGCTG
 AGCACGAGGA CAGCAACTCC TGGGCCGATC CGACCGCCCT ACGGAATGA CCAATCGTCT TACTTAGTGG CTATGCGTCT GCTTGCACTT CGCTGACGAC
 2901 CTGCAAAACG TCTGGACCT GAGCAACAAC ATGAATGGTC TTCGGTTTCC GTGTTTCGTA AAGTCTGGAA ACGCGGAGT CAGCGCCCTG CACCATATG
 GACGTTTTGC AGACGCTGGA CTCGTTGTTG TACTTACCAG AAGCCAAAG CACAAAGCAT TTCAGACCTT TCGGCCCTCA GTGCGGGAC GTGTAATAC
 3001 TTCCGGATCT GCATCGCAGG ATGCTGTGG CTACCTGTG GAACACCTAC ATCTGTATTA ACGAAGCGT GGCATTGACC CTGAGTGATT TTTCTCTGGT
 AAGGCCTAGA CGTAGCGTCC TACGACGACC GATGGACAC CTTGTGGATG TAGACATAAT TGCTTCGGA CCGTAACCTG GACTCACTAA AAAGAGACCA

FIG._25D

3101 CCGCCGCGCAT CCATACCGCC AGTTGTTTAC CCTCACACCG TTCCAGTAAC CGGGCATGTT CATCATCAGT AACCCGTATC GTGAGCATCC TCTCTCGTTT
GGCGCGCGTA GGTATGGCGG TCAACAATG GGAGTGTTGC AAGTTCATTG GCCCGTACAA GTAGTAGTCA TTGGGCATAG CACTCGTAGG AGAGAGCAAA

3201 CATCGGTATC ATTACCCCCA TGAACAGAAA TTCCCCCTTA CACGGAGGCA TCAAGTGACC AAACCGCCCT TAACATGGCC CGCTTTATCA
GTAGCCATAG TAATGGGGGT ACTTGCTCTT AAGGGGGAAT GTGCCTCCGT AGTTCACCTGG TTTGTCTCTT TTTGGCGGGA ATTGTACCGG GCGAAATAGT

3301 GAAGCCAGAC ATTAACGCTT CTGGAGAAAC TCAACGAGCT GGACGGGGAT GAACAGGCAG ACATCTGTGA ATCGCTTCAC GACCACGCTG ATGAGCTTTA
CTTCGGTCTG TAATGGCAA GACCTCTTTG AGTTGCTCGA CCTGCCCTA CTTGTCCGTC TGTAGACACT TAGCGAAGTG CTGGTGGCAG TACTCGAAT

3401 CCGCAGGATC CGGAAATTGT AAACGTTTAT ATTTTCTTAA AATTCGCGTT AATTTTGTGT TAAATCAGCT CATTTTTTAA CCAATAGGCC GAAATCGGCA
GGCGTCTCTAG GCCTTTTAA TTTGCAATTA TAAACAATTT TTAAGCGCAA TTTAAAAACA ATTAGTCTGA GTAAAAAATT GGTATCCGG CTTTAGCCGT

3501 AAATCCCTTA TAAATCAAAA GAATAGACCG AGATAGGTTT GAGTGTGTGT CCAGTTTGA ACAAGAGTCC ACTATTAAAG AACGTGGACT CCAACGTCAA
TTTAGGGAAT ATTTAGTTTT CTATCTGGC TCTATCCAA CTCACAACA GGTCAAACT TGTCTCAGG TGATAATTTC TTGCACCTGA GGTGCACTT

3601 AGGCGGAAA ACCGTCTATC AGGGCTATGG CCCACTAGCT GAACCATCAC CCTAATCAAG TTTTGTGGG TCGAGGTGCC GTAAAGCACT AAATCGGAAC
TCCCGCTTTT TGGCAGATAG TCCCGATACC GGTGTATGCA CTTGTAGTG GGATTAGTTC AAAAAACCC AGCTCCACGG CATTTCTGTA TTTAGCCCTG

3701 CCTAAAGGA CCCCCCGATT TAGAGCTTGA CGGGGAAGC CGCGGAACGT GCGGAGAAAG GAAGGGAAGA AAGCGAAAG AGCGGGCGCT AGGGCGCTGG
GGATTTCCCT CGGGGGCTAA ATCTCGAAT GCGCTTTTC GCGCTTTGA CCGTCTTTTC CTTCCCTTCT TTCGCTTTCC TCGCCCGGGA TCCCGCGACC

3801 CAAGTGAGC GGTACGCTG CGCGTAACCA CCACACCGC CGCGCTTAAT GCGCGCTAC AGGCGCGTC CGGATCCTGC CTCGCGCTT TCGGTGATGA
GTTACATCG CCAGTGGAC GCGCATTTGT GGTGTGGCG GCGGAATTA CGCGCGATG TCCCGCGCAG GCCTAGGACG GAGCGGCAA AGCCACTACT

3901 CGGTGAAAC CTCTGACACA TGCAGCTCCC GGAGACGCTC ACAGCTTGTG TGTAAAGCGA TGCCGGGAGC AGACAAGCCC GTCAGGGGCG GTCAGCGGGT
GCCACTTTG GAGACTGTGT ACGTCGAGG CCTCTGCCAG TGTGAAACAG ACATTCGCCT ACGGCCCTCG TCTGTTCGGG CAGTCCCGG CAGTCGCCCA

4001 GTTGGCGGGT GTCGGGGCGC AGCCATGACC CAGTCACTGA GCGATAGCGG AGTGTATACT GGCTTAAC TA GCGGCATCA GAGCAGATTG TACTGAGAGT
CAACCGCCCA CAGCCCCGCG TCGGTACTGG GTCAGTGCAT CGCTATCGCC TCACATATGA CGAATTGAT ACGCCGTAGT CTCGTCTAAC ATGACTCTCA

FIG._25E

4101 GCACCATATG CGGTGTGAAA TACCGCACAG ATGCGPAAGG AGAAAATACC GCATCAGGCG CTCCTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC
 CGTGGTATAC GCCACACATT ATGGCGTCTC TACGCATTC TCTTTATGG CGTAGTCCG GAGAAGCGA AGGAGCGAST GACTAGCGA CGCGAGCCAG

 4201 GTTCGGCTGC GCGGAGCGGT ATCAGCTCAC TAGTCGAGTG AGTTTCCGCC ATTATGCCAA TAGGTGTCTT AGTCCCCCTAT TCCGTCTCTT CTGTGTACACT CGTTTTCCGG
 CAAGCCGACG CCGCTCGCCA TAGTCGAGTG

 4301 AGCAAAAGGC CAGGAACCGT AAAAAGGCGG CGTTGCTGGC GTTTTTCCTAT AGGTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG
 TCGTTTTCCG GTCCTTGCCA TTTTTCGGC GCAACGACCG CAAAAGGTA TCCGAGGCGG GGGGACTGCT CGTAGTGTTT TTAGCTGCGA GTTCAGTCTC

 4401 GTGGCGAAAC CCGACAGGAC TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GGTCCGACCC TGCCGCTTAC CGGATACCTG
 CACCGCTTG GCGTGTCTG ATATTCTAT GGTCCGCAAA GGGGACCTT CGAGGGAGCA CCGGAGGGA CAAGGCTGG ACGGCGAATG GCCTATGGAC

 4501 TCCGCTTTC TCCCTTCGGG AAGCGTGGG CTTTCTCAT GCTACGCTG TAGGTATCTC AGTTCGGTGT AGTCTGTTG CTCCAAGCTG GGCTGTGTG
 AGCGGGAAG AGGGAAGCCC TTCCGACCGC GAAAGAGTAT CGAGTCCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGGTTCGAC CCGACACACG

 4601 ACGAACCCC CGTTCAGCCC GACCGCTGG CCTTATCCG TAACATCTGT CTTAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC
 TGCTTGGGG GCAAGTCGG CTGGCGACG GGAATAGGCC ATTGATAGCA GAACTCAGGT TGGGCCATT TGTGCTGAAT AGCGGTGACC GTCGTCGGTG

 4701 TGCTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGT GCCTAACTAC GGCTACACTA GAAGGACAGT ATTTGGTATC
 ACCATGTCC TAATCGTCTC GCTCCATACA TCCGCCACGA TGCTCAAGA ACTCACAC CCGATTGATG CCGATGTGAT CTTCCTGTCA TAAACCATAG

 4801 TCGGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC
 ACGGAGACG ACTTCGGTCA ATGGAAGCCT TTTTCTCAAC CATCGAGAAC TAGGCCGTTT GTTTGGTGGC GACCATCGCC ACCAAAAAAA CAAACGTTCG

 4901 AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT
 TCGCTAATG CCGCTCTTTT TTTCTTAGAG TTCTTCTAGG AAACTAGAAA AGATGCCCA GACTGCGAGT CACCTTGCTT TTGAGTGCAA TTCCCTAAAA

 5001 GGTCAATGAGA TTATCAAAAA GGATCTTCAC CTAGATCTT TTAATATAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC
 CCAGTACTCT AATAGTTTTT CCTAGAAGTG GATCTAGGAA AATTAAATTT TTAATTCTAA ATTAGTTAG ATTTCATATA TACTCATTTG AACCAACTG

FIG._25F

5101 AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT TCGTTTCATCC ATAGTTGCCT GACTCCCCCGT CGTGTAGATA ACTACGATAC
 TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGCA GCACATCTAT TGATGCTATG

 5201 GGGAGGGCTT ACCATCTGGC CCCAGTGGTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCAGATTAT ATCAGCAATA AACAGCCAG CCGGAAGGCG
 CCTCCCGGAA TGGTAGACCG GGGTCACGAC GTTACTATGG CGCTCTGGGT GCGAGTGGCC GAGGTCTAAA TAGTCGTTAT TTGGTCGGTC GGCCTTCCCG

 5301 CGAGGCGAGA AGTGGTCCTG CAACTTTATC CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGGCG
 GCTCGCGTCT TCACCAGGAC GTTGAATAG GCGGAGGTAG GTCAGATAAT TAACAACGGC CCTTCGATCT CATTCATCAA GCGGTCAATT ATCAAACGCG

 5401 AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT CGTCGTTTGG TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT
 TTGCAACAAC GGTAAACGAC TCCGTAGCAC CACAGTGCGA GCAGCAAAACC ATACCGAAGT AAGTCGAGGC CAAGGGTTGC TAGTTCCGCT CAATGTACTA

 5501 CCCCCATGTT GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTATTATCA CTCATGGTTA TGGCAGCACT
 GGGGTACAA CACGTTTTTT CGCCAATCGA GGAAGCCAGG AGGCTAGCAA CAGTCTTCAT TCAACCGGCG TCACAATAGT GAGTACCAAT ACCGTCGTGA

 5601 GCATTAATCT CTACTGTCA TGCCATCCGT AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGATGCG GCGACCGAGT
 CGTATTAGA GAATGACAGT ACGGTAGGCA TTCTACGAAA AGACACTGAC CACTCATGAG TTGGTTCAGT AAGACTCTTA TCACATACGC CGCTGGCTCA

 5701 TGCTCTTGGC CGGCGTCAAC ACGGATTAAT ACCGCGCCAC ATAGCAGAAC TTTTAAAGTG CTCATCATTG GAAACGTTTC TTCGGGGCGA AAACCTCAA
 ACGAGAACGG GCGGCAGTTG TGCCCTATTA TGGCGCGGTG TATCGTCTTG AAATTTTAC GAGTAGTAAC CTTTTGCAAG AAGCCCCGCT TTTGAGAGTT

 5801 GGATCTTACC GGTGTGAGA TCCAGTTCGA TGTAACCCAC TCGTGACCC AACGATCTT CAGCATCTTT TACTTTCACC AGCGTTTCTG GGTGAGCAAA
 CCTAGAATGG CGACAACCTCT AGGTCAAGCT ACATTGGGTG AGCACGTGGG TTGACTAGAA GTCGTAGAAA ATGAAAGTGG TCGCAAGAC CCACTCGTTT

 5901 AACAGGAAG CAAATGCCG CAAAAAGGG AATAAGGGG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG
 TTGTCTCTCC GTTTTACGGC GTTTTTTCCC TTATTCCCCT TGTCCTTTA CAACCTATGA GTATGAGAAG GAAAAAGTTA TAATACTTC GTAAATAGTC

 6001 GGTATTGTC TCATGAGCGG ATACATATTT GAATGATTTT AGAAAAATAA ACAATAGGG GTTCCCGGCA CATTTCCTCCG AAAAGTGCCA CCTGACGCT
 CCAATAACAG AGTACTCGCC TATGTATAAA CTTACATAAA TCTTTTTTATT TGTTTATCCC CAAGCGCGGT GTAAAGGGGC TTTCACGGT GGACTGCAGA

FIG._25G

6101 AAGAAACCAT TATTATCATG ACATTAAACCT ATAAAAATAG GCGTATCAGG AGGCCTTTC GTCTTCAATA CAGGTAGACC TTTCGTAGAG ATGTACAGTG
TTCTTTGGTA ATAAATAGTAC TGTAATTGGA TATTTTATC CGCATAGTGC TCCGGAAAG CAGAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTAC

6201 AAATCCCCGA AATTATACAC ATGACTGAAG GAAGGGAGGT CGTCATTCCC TGCCGGGTTA CGTCACCTAA CATCACTGTT ACTTTAAAAA AGTTTCCACT
TTTAGGGGCT TTAATATGTG TACTGACTTC CTTCCCTCGA GCAGTAAGGG ACGGCCCAAT GCAGTGGATT GTAGTGACAA TGAAATTTTT TCARAGGTGA

6301 TGACACTTTG ATCCCTGATG GAAAACGCAT AATCTGGGAC AGTAGAAGG GCTTCATCAT ATCAAAATGCA ACGTACAAAG AAATAGGGCT TCTGACCTGT
ACTGTGAAC TAGGGACTAC CTTTGGCGTA TTAGACCCCTG TCATCTTTCC CGAAGTAGTA TAGTTTACGT TGCATGTTTC TTTATCCCGA AGACTGGACA

6401 GAAGCAACAG TCAATGGGCA TTTGTATAAG ACAACATATC TCACACATCG ACAACCAAT ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGTGAAT
CTTCGTTGTC AGTTACCCGT AAACATATTC TGTTTGATAG AGTGTGAGC TGTTTGGTTA TGTTATGTCC ATCTGGAAAG CATCTCTACA TGTCACTTTA

6501 CCCGAAATT AFACACATGA CTGAAGGAAG GGAGCTCGTC ATTCCCTGCC GGGTTACGTC ACCTAACATC ACTGTTACTT TAAAAAAGTT TCCACTTGAC
GGGGCTTAA TATGTGTACT GACTTCCTTC CCTCGAGCAG TAAGGGACGG CCCAATGCAG TGGATGTAG TGACAATGAA ATTTTTCAA AGGTGAACTG

6601 ACTTTGATCC CTGATGGAA ACGCATATC TGGGACAGTA GAAAGGGGTT CATCATATCA AATGCAACGT ACAAGAAT AGGGCTTCTG ACCTGTGAAG
TGAACACTAGG GACTACCTTT TCGGTATTAG ACCCTGTCAI CTTTCCCGAA GTAGTATAGT TTACGTTGCA TGTTTCTTTA TCCCGAAGAC TGGACACTTC

6701 CAACAGTCAA TGGGCATTG TATAAGACAA ACTATCTCAC ACATCGACAA ACCAATACAA TCTACAGGTA GACCTTTCGT AGAGATGTAC AGTGAATCC
GTTGTCAGTT ACCCGTAAAC ATATTCTGTT TGATAGAGTG TGTAGCTGTT TGTTATGTT AGATGTCCAT CTGGAAAGCA TCTCTACATG TCACTTTAGG

6801 CCGAAATTAT ACACATGACT GAAGGAAGGG AGCTCGTCAT TCCCTGCGG GTTACGTCAC CTAACATCAC TGTTACTTTA AAAAAGTTTC CACTTGACAC
GGCTTTAATA TGTGTACTGA CTTCTTCCC TCGAGCAGTA AGGGACGGCC CAATGCAGTG GATTGTAGTG ACAATGAAAT TTTTTCAAAG GTGAACCTGT

6901 TTTGATCCCT GATGGAAAAC GCATAATCTG GGACAGTAGA AAGGGCTTCA TCATATCAA TGCAACGTAC AAAGAATAG GGCTTCTGAC CTGTGAAGCA
AACTAGGGA CTACCTTTTG CGTATTAGAC CCTGTCTATCT TTCCCGAAGT AGTATAGTTT ACGTGTCATG TTTCTTTATC CCGAAGACTG GACACTTCGT

7001 ACAGTCAATG GGCATTGTA TAAAGACAAAC TATCTCACAC ATCGACAAAC CAATACAATC
TGTCAGTTAC CCGTAAACAT ATTCTGTTTG ATAGAGTGTG TAGCTGTTTG GTTATGTTAG

FIG.. 25H

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1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAGAAGA AGAGTCGAAT
  CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGCTCTG TACTTTTITAG AGTAACGACT CAACAATAAA TTGGAACGGG TTTTCTTCTT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACACGG GTTGATTGAT CAGGTAGAGG
  CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTITAC TGGTTGTCGC CAACTAATA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAG CCCGATGCCA GCATTCTCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
  CCGCGGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCCTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCACA GCTGTCTATA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTITAT TTTTAATGTA TTTGTAATA GTACGCAAGT
  TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAATA AGGTATGTA GAGGTGAGG TGATTTTATG AAAAGAATA TCGCATTTCT TCTTGCATCT ATGTTCTGTTT TTTCTATTGC TACAAATGCC
  AGTGCATTTT TCCCATACAT CTCCAATCC ACTAAAATAC TTTTCTTAT AGCGTAAAGA AGAAGCTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG

1 M K K N I A F L L A S M F V F S I A T N A
  ^start of stII sequence

501 TATGCATCCG ATATCCAGAT GACCCAGTCC CCGAGTCCC TGTCGGCTC TGTCGGCGAT AGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTCTCCA
  ATACGTAGGC TATAGGTCTA CTGGGTGAGG GGCTCGAGG ACAGCGGAG ACACCCGCTA TCCCAGTGGT AGTGGACGGC ACGTCTAGTC CTACACAGGT

22 Y A S D I Q M T Q S P S L S A S V G D R V T I T C R A S Q D V S T
  ^light chain start ^CDR-L1

601 CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAAGTCC GAAGTTCTG ATTTACTCGG CATCCTTCTC CTACTCTGGA GTCCCCTTCTC GCTTCTCTGG
  GACGACATCG GACCATAGTT GTCTTTGCTC CTTTTCGAGG CTTTCAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAGAG CGAAGAGACC

56 A V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G
  ^CDR-L2

701 TAGCGGTTCC GGGACGGATT TCACTCTGAC CATCAGCAGT CTGACGCCGG AAGACTTCG AACTTATTAC TGTACGCAAT CTTATACTAC TCCTCCCACG
  ATCGCCAAGG CCCTGCCTAA AGTGAGACTG GTAGTCTGTA GACGTCGGCC TTTTGAAGCG TTGAATAATG ACAGTCGTTA GAATATGATG AGGAGGTGC

89 S G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T
  ^CDR-L3

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FIG._26A

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801 TTCCGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG CTGCACCATC TGTCTTCAFC TTCCCGGCAT CTGATGAGCA GTTGAAATCT GGAAGTGCCT
AAGCCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC GACGTGGTAG ACAGAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGGA
122 F G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S

901 CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC CAAAGTACAG TGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTAC
GACAACACAC GGACGACTTA TTGAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA TTGAGGGTCC TCTCACAGTG
156 V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T

1001 AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC ACCCTGAGC TGAGCAAAGC AGACTAGCAG AAACACAAAG TCTAGCCCTG CGAAGTCAAC
TCTCGTCTGT TCGTTCTCTGT CGTGCATGTC GGAGTCGTGC TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG
189 E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T

1101 CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTCAACA GGGGAGAGTG TGGTGCCAGC TCCGGATGG CTGATCCGAA CCGTTTCCGC GGTAAAGGACC
GTAGTCCCGG ACTCGAGCGG GCAGTGTTC TCGAAGTTGT CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAAAGCG CCATTCTCTGG
222 H Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L
^end of light chain, start of gD tag

1201 TGGCAATCACT CGAGGCTGAT CCTCTACGCC GGACGCATCG TGGCCCTAGT ACACAAGTTC ACGTAAAAG GGTAACTAGA GGTGAGGTG ATTTATATGAA
ACCGTATTGA GCTCCGACTA GGAGATGCGG CCGCGTAGC ACCGGGATCA TCGGTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAATACTT
256 A O
^start of stII

1301 AAAGAATATC GCATTCTTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGGCTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG
TTTCTTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTGGCGAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCAC
-21 K N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G L V
^start of heavy chain

1401 CAGCCAGGGG GCTCACTCCG TTTGTCCTGT GCAGCTTCTG GCTTCAACAT TAAAGACACC TATAVACACT GGTGCGTCA GGCCCCGGGT AAGGGCCTGG
GTGCGTCCCC CGAGTGAGGC AAACAGGACA CGTCGAAGAC CGAAGTTGTA ATTTCTGCG ATATATGTGA CCCAGCAGT CCGGGGCCCA TTCCCGGACC
13 Q P G G S L R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E
^CDR-H1

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FIG._26B

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1501 AATGGGTTGC AAGGATTAT CCTACGAATG GTTATACTAG ATATGCCGAT AGCGTCAAGG GCCGTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC
TTACCCAACG TTCTTAATAA GGATGCTTAC CAATGCTTAC TATACGGCTA TCGCAGTTCC CGGCAAGTG ATATTCCGGT CTGTGTAGGT TTTTGTGTGG
47 W V A R I Y P T N G Y T R Y A D S V K G R F T I S A D T S K N T A
^CDR-H2

1601 CTACCTACAA ATGAACAGCT TAAGAGTGA GGACACTGCC GTCTATTATT GTAGCCGCTG GGGAGGGGAC GGCTTCTATG CTATGGACTA CTGGGGTCAA
GATGGATGTT TACTTGTGCA ATTCTCGACT CCTGTGACGG CAGATAATAA CATCGGGGAC CCTTCCCCTG CCGAAGATAC GATACCTGAT GACCCAGTT
80 Y L Q M N S L R A E D T A V Y Y C S R W G G D G F Y A M D Y W G Q
^CDR-H3

1701 GGAACACTAG TCACCGCTC CTCGGCCTCC ACCAAGGGCC CATCGGTCTT CCCCTTGGCA CCTCTCTCCA AGAGCACTC TGGGGGCACA GCGGCCCTGG
CCTTGTGATC AGTGGCAGAG GAGCCGGAGG TGGTTCCCGG GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGACC
113 G T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G

1801 GCTGCCTGGT CAAGGACTAC TTCCCGGAAC CGGTGACGGT GTCGTGGAAC TCAGGCGCCC TGACCAGCGG CGTGCAACACC TTCCGGGCTG TCCTACAGTC
CGACGGACCA GTTCTGTGAG AAGGGGCTTG GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGGTCGCC GCACGTTGG AAGGCCGAC AGGATGTGAG
147 C L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S

1901 CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACCGTGCCC TCCAGCAGCT TGGGCACCCA GACCTACATC TGCAACCTGA ATCACAAGCC CAGCAACACC
GAGTCCTGAG ATGAGGGAGT CGTCGCACCA CTGGCAGCGG AGTCTGTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTGG
180 S G L Y S L S S V V T V P S S L G T Q T Y I C N V N H K P S N T

2001 AAGGTCGACA AGAAGTTGA GCCCAATCT TGTGACAAA CTCACGGCCG CATGAACAG CTAGAGGACA AGGTCGAAGA GCTACTCTCC AAGAACTACC
TTCCAGCTGT TCTTTCACT CGGGTTTAGA ACACTGTTTT GAGTCCCGGC GTACTTTGTC GATCTCCTGT TCCAGCTTCT CGATGAGAGG TTCTTGATGG
213 K V D K K V E P K S C D K T H G R M K Q L E D K V E L L S K N Y H
^end of heavy chain, start of leucine zipper

2101 ACCTAGAGAA TGAAGTGCA AGACTCAAAA AACTTGTGCG GGAGCGCGGA AAGCTTAGTG CCGGTGGCTC TGGTCCCGT GATTTTGATT ATGAAAAGAT
TGGATCTCTT ACTTCACCGT TCTGAGTTTT TTGAACAGCC CCTCGCGCCT TTGCAATCAC CGCCACCGAG ACCAAGGCCA CTAATACTAA TACTTTTCTA
247 L E N E V A R L K K L V G E R G K L S G G S G S G D F D Y E K M
^end of leucine zipper, start of gene III coat protein (267-end)^

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FIG._26C

2201 GGCAACCGCT AATAAGGGG CTATGACCGA AATGCCGAT GAAAACGGC TACAGTCTGA CGCTAAAGC AAACATGATT CTGTCGCTAC TGATTACGGT
 CCGTTTGGGA TTATTCCCC GATACTGGCT TTATACGGCTA CTTTGGCGG ATGTCAGACT CGGATTTCCG TTGTGACTAA GACAGCGATG ACTAATGCCA
 280 A N A N K G A M T E N A D E N A L Q S D A K G K L D S V A T D Y G
 2301 GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCTTG CTAATGGTAA TGGTGCTACT GGTGATTTG CTGGCTCTAA TTCCCAAATG GCTCAAGTCG
 CGACGATAGC TACCAAGTA ACCACTGCAA AGGCCGGAAC GATTACCAAT ACCACGATGA CCCTAAAC GACCGAGATT AAGGTTTAC CGAGTTCAGC
 313 A A I D G F I G D V S G L A N G N G A T G D F A G S N S Q M A Q V G
 2401 GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA ATATTACCT TCCCTCCCTC AATCGGTTGA ATGTCGCCCT TTGTCTTTA GCGTGGTAA
 CACTGCCACT ATTAAGTGA AATTACTTAT TAAAGGCAGT TATAAATGGA AGGAGGGAG TTAGCCACT TACAGCGGA AAACAGAAAT CGCGACCAT
 347 D G D N S P L M N N F R Q Y L P S L P Q S V E C R P F V F S A G K
 2501 ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACTTA TTCCGTGGTG TCTTTGCGTT TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTCTACG
 TGGTATACTT AAGAGATAAC TAACACTGTT TTATTGTAAT AAGGCACCAC AGAAACGCAA AGAAATATA CAACGGTGA AATACATACA TAAAGATGC
 380 P Y E F S I D C D K I N L F R G V F A F L L Y V A T F M Y V F S T
 2601 TTTGTACA TACTGCGTAA TAAGGAGTCT TAATCATGCC AGTTCTTTTG GCTAGCGCG CCTATACCT TGTCGCTC CCCGGGTGC GTCCGGGTGC
 AAACGATTGT ATGACGCATT ATTCCTCAGA ATTACTACGG TCAAGAAAC CGATCGCGC GGGATATGGA ACAGACGGAG GGGCGCAACG CAGCGCCACG
 413 F A N I L R N K E S O
 2701 ATGGAGCCG GCCACCTCGA CCTGAATGGA AGCCGCGGC ACCTCGCTAA CGGATTACCC ACTCCAAGAA TTGGAGCCAA TCAATTCTTG CGGAGAACTG
 TACCTCGGC CCGTGGAGCT GGACTTACCT TCGGCGCGC TGGAGCGATT GCCTAAGTGG TGAGGTTCTT AACCTCGGT AGTTAAGAAC GCCTCTTGAC
 2801 TGAATGCGCA AACCAACCCT TGGCAGAACA TATCCATCGC GTCCGCCATC TCCAGCAGCC GCACGCGCG CATCTCGGC AGCCTGGGT CCTGGCCACG
 ACTTACGGT TTGGTTGGGA ACCGCTTGT ATAGTAGCG CAGGCGGTAG AGGTGCTCG CGTGCGCGC GTAGAGCCG TCGCAACCCA GGACCGGTGC
 2901 GGTGCGCATG ATCGTGTCC TGTCGTTGAG GACCCGGCTA GGCTGGCGG GTTGCTTAC TGGTTAGCAG AATGAATCAC CGATACCGA GCGAACGTGA
 CCACGCGTAC TAGCACGAG ACAGCAACTC CTGGCCGAT CGACCGCC CAACGGAATG ACCAATCGTC TTACTTAGTG GCTATCGCT CGCTGCACT
 3001 AGCGACTGCT GCTGCAAAAC GTCTGCGACC TGAGCAACAA CATGAATGTT CTTCGGTTTC CGTGTTCCT AAAGTCTGGA AACCGGAAG TCAGCGCCCT
 TCGCTGACGA CGACGTTTG CAGACGCTGG ACTCGTTGTT GACTTACCA GAAGCCAAAG GCACAAAGCA TTTCAGACCT TTGCGCTTC AGTCGGGGA

FIG._26D

3101 GCACCATAT GTTCCGGATC TGCATCCGAG GATGCTGCTG GCTACCCCTGT GGRACACCTA CATCTGTATT AACGAAGCG TGGCATTTGAC CCTGAGTGAT
CGTGGTAATA CAAGGCCTAG ACGTAGCGTC CTACGACGAC CGATGGGACA CCTGTGGAT GTAGACATAA TTGCTTCGG ACCGTAAC TG GACTCACTA

3201 TTTTCTCTGG TCCCGCCGCA TCCATACCGC CAGTTGTTTA CCTCACAAC GTTCCAGTAA CCGGGCATGT TCATCATCAG TAACCCGTAT CGTGAGCATC
AAAAGAGACC AGGGCGCGT AGGTATGGC GTCAACAAT GGGAGTGTG CAAGTCAAT GGCCCGTACA AGTAGTAGTC ATTGGGCATA GCACTCGTAG

3301 CTCTCTCGTT TCATCGGTAT CATTACCCCT CATTAACGAA ATTCCCCCTT ACACGGAGG ATCAAGTGAC CAAACAGGAA AAAACCGCC TTAACATGGC
GAGAGAGCAA AGTAGCCATA GTAATGGGG TACTTGTCTT TAAGGGGAA TGTGCTCCG TAGTTCAC TGTTGTCTT TTTTGGCGG AATTGTACCG

3401 CCGCTTTATC AGAAGCCAGA CATTAACGCT TCTGGAGAAA CTCACAGAGC TGGACCGCGA TGAACAGGCA GACATCTGT AATCGCTTCA CGACCACGCT
GGCGAAATAG TCTTCGGTCT GTAATTGCCA AGACCTCTTT GAGTTGCTCG ACCTGGCCT ACTGTCCGT CTGTAGACAC TTAGCGAAGT GCTGGTGGCA

3501 GATGAGCTTT ACCGCAGGAT CCGGAAATTG TAAACGTTAA TATTTTGTTA AAATTCGCGT TAAATTTTG TTAATCAGC TCATTTTTTA ACCAATAGGC
CTACTCGAAA TGGCGTCTTA GGCTTTTAA ATTTGCAAT ATAAACAAT TTTAAGCGCA ATTTAAAC AATTAGTTC AGTAAAAAT TGGTTATCCG

3601 CGAATCGGC AAAATCCCTT ATAAATCAA AGAATAGACC GAGATAGGTT TGAGTGTGT TCCAGTTTG AACAAAGATC CACTATTAAA GAACGTGGAC
GCTTAGCCG TTTTAGGGAA TATTTAGTT TCTTATCTGG CTCATATCCA ACTCACAACA AGTCAAAACC TTGTTCTCAG GTGATAATTT CTTCACCTG

3701 TCCAACGTCA AAGGGCGAAA AACCGTCTAT CAGGGCTATG GCCACTACG TGAACCATCA CCTAATCAA GTTTTTTGGG GTCGAGGTGC CGTAAAGCAC
AGGTGTCAGT TTCCCGCTTT TTGGCAGATA GTCCCGATAC CGGGTATGC ACTTGGTAGT GGGATTAGTT CAAAAAACCC CAGCTCCAG GCATTTCTGTG

3801 TAAATCGGA CCTAAAGG AGCCCCCGAT TTAGAGCTTG ACGGGGAAAG CCGCGGAACG TGCGGAGAAA GGAAGGGAAG AAAGCGAAA GAGCGGGCGC
ATTTAGCCTT GGATTTCCC TCGGGGGCTA ATCTCGAAC TGCCCCCTTC GGCGCTTGC ACCGCTCTTT CCTTCCCTTC TTTCGCTTTC CTCGCCCGCG

3901 TAGGGCGCTG GCAAGTGTA CCGTCACGCT GCGCGTAACC ACCACACCCG CCGCGCTTAA TCGCGCGCTA CAGGGCGCGT CCGGATCCTG CCTCGCGCGT
ATCCCGGAC CGTTCACATC GCCAGTCCA CCGCATTTG TGGTGTGGG GCGCGGAATT ACGGGCGAT GTCCCGGCA GGCCTAGGAC GGAGCGCGCA

4001 TTCGGTGATG ACGGTGAAA CCTCTGACAC ATGCAGTCC CCGAGACGGT CACAGCTGT CTGTAAGCG ATGCCGGGAG CAGACAAGCC CGTCAGGGCG
AAGCCACTAC TGCCACTTT GGAGACTGT TACGTGAGG GCCTCTGCCA GTGTGGAACA GACATTCGCC TACGGCCCTC GTCTGTTCG GCAGTCCCGC

4101 CGTCAGCGG TGTGGCGGG TGTCCGATG CAGCCATGAC CCAGTCAGT AGCGATAGCG GAGTGTATAC TGGCTTAAT ATCGGGCATC AGAGCAGATT
GCACTCGCC ACAACCGCC ACAGCCCCG GTCGGTACTG GGTCACTGCA TCGCTATCGC CTCACATATG ACCGAATTGA TACGCCGTAG TCTCGTCTAA

FIG._26E

4201 GTACTGAG TGCACCATAT GCGGTGTGAA ATACCGCACA GATCGGTAAG GAGAAAATAC CGCATCAGGC GCTCTTCCGC TTCTTCGGTC ACTGACTCGC
CATGACTCTC ACGTGGTATA CGCCACACTT TATGGCGTGT CTACGCCATT CTCTTTTATG CGGTAGTCCG CGAGAGCGG AAGGAGCGAG TGACTGAGCG

4301 TCGGCTCGGT CGTTCGGCTG CGCGGAGCGG TATCAGCTCA CTCAAAGCG GTAATACGGT TATCCACAGA ATCAGGGGAT AACGAGGAA AGAACATGTG
ACGCGAGCCA GCAAGCGGAC GCCGCTGCC ATAGTCTGAGT GAGTTTCCGC CATTATGCCA ATAGGTCTCT TAGTCCCTTA TTGCGTCTCTT TCTTGATACAC

4401 AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAAGGCC GCGTTGCTGG CGTTTTCCTCA TAGGCTCCGC CCCCCTGACG AGCATCACAA AAATCGACGC
TCGTTTTCGG GTCGTTTTCG GGTCTTTGGC ATTTTTCGG CGCAACGACC GCAAAAAGGT ATCCGAGCGG GGGGACTGC TCGTAGTGTT TTTAGCTGCG

4501 TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA
AGTTCAGTCT CCACCGCTTT GGGCTGTCTT GATATTCTA TGGTCCGCAA AGGGGACCT TCGAGGAGC ACGGAGAGG ACAAGGCTGG GACGGCGAAT

4601 CCGGATACCT GTCGGCTTT CTCCTTCGG GAAGCGTGGC GCTTCTCAT AGCTCACGCT GTAGGTATCT CAGTTCGGTG TAGTCTGTTT GCTCCAAGCT
GGCCTATGGA CAGGCGAAA GAGGAAGCC CTTGCAAGC TTTGCAAGTA TCGAGTGGA CATCCATAGA GTCAAGCCAC ATCCAGCAAG CGAGGTTTCA

4701 GGGCTGTG CACGAACCC CGGTTTCAGC CGCTTATCCG GTAACATACG TCTTGTACTCC AACCCGGTAA GACACGACTT ATGCCACTG
CCCGACACAC GTGCTTGGG GGCAGTCCG GCTGGCGACG CGGAATAGGC CATTGATAGC AGAATCAGG TTGGGCCATT CTGTGCTGAA TAGCGGTGAC

4801 GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC TACAGATTC TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG
CGTCGTCGGT GACCAATGTC CTAATCTGCT CAGTCCATAC ATCCGCCACG ATGTCTCAAG AACTTCACCA CCGGATGAT GCCGATGTA TCTTCTCTGTC

4901 TATTGTGAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAAGATT GGTAAGTCTT GATCCGGCAA ACAAAACCACC GCTGGTAGCG GTGGTTTTT
ATAAACCATTA GACGCGAGAC GACTTCGGTC AATGGAAGCC TTTTCTCAA CCATCGAGAA CTAGGCCGTT TGTTTGGTGG CGACCATCGC CACCAAAAAA

5001 TGTTCGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGG TCTGACGCTC AGTGAACGA AACTCACGT
ACAAACGTC GTCGCTAAT GCGGCTCTTT TTTTCTCTAGA GTTCTCTTAG GAAACTAGAA AAGATGCCCC AGACTGCCAG TCACCTTGCT TTTGAGTGCA

5101 TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT TTTAAATTA AAATGAAGTT TTAATCAAT CTAAAGTATA TATGAGTAA
ATTCCCTAAA ACCAGTACT TAATAGTTTT TCCTAGAAAT GGATCTAGGA AAATTTAAT TTTACTTCAA AATTAGTTA GATTTCATAT ATACTCATTT

5201 CTTGGTCTGA CAGTTTACAA TGCTTAATCA GTGAGGCACC TATCTCAGG ATCTGTCTAT TTCGTTTCATC CATAGTTGCC TGACTCCCCG TCGTGTAGAT
GAACCACT GTCATGGTT ACGAATTAGT CACTCCGTGG ATAGATCTGC TAGACAGATA AAGCAAGTAG GTATCAACGG ACTGAGGGGC AGCAGATCTA

FIG._26F

5301 AACTACGATA CGGGAGGGCT TACCATCTGG CCCAGTGTCT GCAATGATAC CGCGAGACCC AGGCTCACCG GCTCCAGATT TATCAGCAAT AAACCAGCCA
TTGATGCTAT GCCCTCCCGA ATGGTAGACC GGGGTACCGA CGTTACTATG GCGTCTGGG TCGGAGTGGC CGAGGTCTAA ATAGTCGTTA TTTGGTCCGT

5401 GCGGGAAGG CCGAGCGCAG AAGTGGTCTT GCAACTTTAT CCGCTCCCAT CCAGTCTATT AATTGTTGCC GGAAGCTAG AGTAAGTACT TCGCCAGTTA
CGGCTTCCC GGCTCGGTC TTCACCAGGA CGTTGAATA GCGGAGGTA GGTGAGATA TTAACAACGG CCCTTCGATC TCATTCAATCA AGCGGTCAAT

5501 ATAGTTTGG CAACGTTGTT GCCATTGCTG CAGGCATCGT GGTGTACGC TCGTGTGTTG GTATGGCTTC ATTCAGCTCC GGTCCCAAC GATCAAGGCG
TATCAAACGC GTTGCAACAA CGGTAACGAC GTCCGTAGCA CCACAGTGG AGCAGCAAC CATACCGAAG TAAGTCGAGG CCAAGSGTTG CTAGTCCGC

5601 AGTTACATGA TCCCCCATGT TGTGCAAAA AGCGGTTAGC TCCTTCGGTC CTCCGATCGT TGTGAGAAGT AAGTTGGCCG CAGTGTATC ACTCATGGTT
TCAATGTACT AGGGGTACA ACAGTTTTT TCGCCCATCG AGAAGCCAG GAGGTAGCA ACAGTCTTCA TTCAACCGGC GTCACAATAG TGAGTACCAA

5701 ATGGCAGCAC TGCATAATC TCCTACTGTC ATGCCATCCG TAAGATGCTT TTCGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC
TACCGTCGTG ACGTATTAG AGAATGACAG TACGGTAGG AATCTACGAA AAGACACTGA CCACCTCATGA GTTGGTTCAG TAAGACTCTT ATCACATACG

5801 GCGCACCGAG TTGCTCTTGC CCGCGGTCAA CACGGGATAA TACCGGCCCA CATACAGAA CTTTAAAAGT GCTCATCATT GGAACACGTT CTTCGGGGCG
CCGCTGGCTC AACGAGAAG GCGCGCAGTT GTGCCCTATT ATGGCGCGGT GTATCGTCTT GAAATTTTCA CGAGTAGTAA CCTTTTGCAA GAAGCCCCGC

5901 AAAACTCTCA AGGATCTTAC CGCTGTTGAG ATCCAGTTTG ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTTAC CAGCGTTTCT
TTTTGAGAGT TCCTAGAATG GCGACAACTC TAGGTCAAGC TACATTGGGT GAGCACGTGG GTTGACTAGA AGTCGTAGAA AATGAAAGTG GTCGCAAGA

6001 GGGTGAGCAA AAACAGGAAG GCAAAATGCC GAATAAGGC GACACGGAA TGTGAATAC TCATACTCTT CCTTTTCAA TATTATTGAA
CCCACTCGTT TTTGTCCCTC CGTTTTACGG CGTTTTTCC CTATTCCCG CTGTCCCTTT ACAACTTATG AGTATGAGAA GGAATAAGTT ATAATACTT

6101 GCATTATCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT TAGAAAAATA AACAAATAGG GGTCCCGCGC ACATTTCCCG GAAAAGTGCC
CGTAAATAGT CCCAATAACA GAGTACTCGC CTATGTATAA ACTTACATAA ATCTTTTAT TTGTTTATCC CCAAGGCGCG TGTAAGGGG CTTTTACGG

6201 ACCTGACGTC TAAGAAACCA TTATTATCAT GACATTACC TATAAAATA GCGGTATCAC GAGGCCCTTT CGTCTTCAAT ACAGGTAGAC CTTTCGTAGA
TGGACTGCAG ATTCTTTGGT AATAATAGTA CTGTAATGG ATATTTTTAT CCGCATAGTG TCCTCGGAAA GCAGAAAGTTA TGTCCATCTG GAAAGCATCT

6301 GATGTACAGT GAAATCCCG AAATTATACA CATGACTGAA GGAAGGAGC TCGTCATTCC CTGCCGGGT AGCTACCTA ACATCACTGT TACTTTAAA
CTACATGTCA CTTTAGGGC TTTAATATGT GTACTGACTT CCTTCCCTCG AGCACTAAGG GACGGCCCAA TGCAGTGGAT TGTAAGTACA ATGAAATTTT

FIG._26G

6401 AAGTTTCCAC TTGACACTTT GATCCCTGAT GGAAGCGA TAATCTGGGA CAGTAGAAG GGCTTCATCA TATCAATGC AACGTACAAA GAAATAGGGC
TTCAAAGGTG AACTGTGAAA CTAGGGACTA CCTTTTGGGT ATTAGACCCCT GTCATCTTTC CCGAAGTAGT ATAGTTTACG TTGCATGTTT CTTTATCCCC

6501 TTCTGACCTG TGAAGCAACA GTCATATGGG ATTTGTATAA GACAAACTAT CTCACACATC GACAAACCAA TACAATACAG GTAGACCTTT CGTAGAGATG
AAGACTGGAC ACTTCGTGTG CAGTTACCCG TAAACATATT CTGTTTGATA GAGTGTGTAG CTGTTTGTTT ATGTTATGTC CATCTGGAAA GCATCTCTAC

6601 TACAGTGAAA TCCCCGAAAT TATACACATG ACTGAAGGAA GGGAGCTCGT CATTCCTGCG CGGGTTACGT CACCTAACAT CACTGTTACT TTAATAAAGT
ATGTCACCTT AGGGGCTTIA ATATGTGTAC TGACTTCCTT CCTCGAGCA GTAAGGGACG GCCCAATGCA GTGGATTGTA GTGACAATGA AATTTTITCA

6701 TTCCACTTGA CACTTTGATC CCTGATGGAA AACGCATAAT CTGGGACAGT AGAAGGGCT TCATCATATC AAATGCAACG TACAAGAAA TAGGGCTTCT
AAGGTGAACT GTGAATACTAG GGACTACCTT TTCCGTATTA GACCTGTCA TCTTCCCCGA AGTAGATAG TTTTACGTTGC ATGTTCTTTT ATCCCGAAGA

6801 GACCTGTGAA GCAACAGTCA ATGGGCATTT GTATAAGACA AACTATCTCA CACATCGACA AACCAATACA ATCTACAGGT AGACCTTTTC TAGAGATGTA
CTGGACACTT CGTTGTGAGT TACCCGTAAA CATATTCTGT TTGATAGAGT GTGTAGCTGT TTGGTTATGT TAGATGTCCA TCTGGAAAAGC ATCTCTACAT

6901 CAGTGAATC CCCGAAATTA TACACATGAC TGAAGGAAGG GAGCTCGTCA TTCCCTGCGG GGTACCTCA CCTAACATCA CTGTTACTTT AAAAAAGTTT
GTCACITTAG GGGCTTTAAT ATGTGTACTG ACTTCCTTCC CTCGAGCAGT AAGGGACGGC CCAATGCAGT GGATTGTAGT GACAATGAAA TTTTITCATA

7001 CCACTTGACA CTTTGTATCC TGATGGAAA CGCATAATCT GGGACAGTAG AAAGGGCTTC ATCATATCAA ATGCCACGTA CAAAGAAATA GGGCTTCTGA
GGTGAAGTGT GAAACTAGGG ACTACCTTTT GCGTATTAGA CCCTGTCTATC TTTCCCGAAG TAGTATAGTT TACGTGTCAT GTTCTTTTAT CCGAAGACT

7101 CCTGTGAAGC AACAGTCAAT GGGCATTGT ATAAGACAAA CTATCTACA CATCGACAAA CCAATACAAT C
GGACACTTCG TTGTCACTTA CCCGTAACA TATTCTGTTT GATAGAGTGT GTAGCTGTTT GGTATGTTA G

FIG._26H

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1  ATGAAAGA ATATCGGATT TCTTCTTGCA TCATATGTTG TTTTCTCTAT TGCTACAAAT GCCTATGAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC
   TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTC TATAGTCTA CTGGTTCAGG GGCTCGAGGG
1  M K K N I A F L L A S M F V F S I A T N A Y A D I Q M T Q S P S S L
   ^met
   ^start of stII signal sequence
   ^start of light chain

101 TGTCGGCTC TGTTGGGGAT AGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTGTCCA CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAGCTCC
   ACAGGGGAG ACACCCGCTA TCCAGTGGT AGTGGACGGC ACGGTACGTC CTACACAGGT GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG
35  S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P
   ^CDR-L1

201 GAAGCTTCTG ATTTACTCGG CATCCTTCCT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG TAGCGGTCC GGGACGGATT TCACTCTGAC CATCAGCAGT
   CTTGGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAGAG CGAAGAGACC ATCGCCAGG CCCTGCCATA AGTGAGACTG GTAGTCGTCA
68  K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S S
   ^CDR-L2

301 CTGCAGCGG AGACTTCGC AACTTATTAC TGTGAGCAAC ATTATACTAC TCCTCCACG TTCGGACAGG GTACCAAGGT GGAGATCAA CGAACTGTGG
   GACGTCGGC TTCTGAAGCG TTGAATAATG ACAGTCGTTG TAATATGATG AGGAGGTGC AAGCCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC
101 L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T V A
   ^CDR-L3

401 CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAATCT GGAATGCCT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC
   GACGTGGTAG ACAGAACTAG AAGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGGA GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG
135  A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A

501 CAAAGTACAG TGAAGGTGG ATACGCCCT CCATCGGGT AACTCCAGG AGAGTGTAC AGAGCAGGAC AGCAAGACA GCACCTACAG CCTCAGCAGC
   GTTTCATGTC ACCTTCACC TATTGCGGGA GGTAGGCCA TTGAGGGTCC TCTCACAGTG TCTCGTCTG TCGTCTCTGT CGTGGATGTC GGAGTCGTGCG
168  K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGAGC TGAGCAAGC AGACTACGAG AAACACAAG TCTACGCCCTG CGAAGTCACC CATCAGGSCC TGAGCTGCC CGTCACAAAG AGCTTCAACA
   TGGGACTCGG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATCGGAC GCTTCAGTGG GTAGTCCCGG ACTCGAGCGG GCAGTGTTC TCGAAGTTGT
201 T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R

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FIG.-27A

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701 GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAAGACC TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGCATCG
CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAAGCGG CCATTCCTGG ACCGTATTGA GCTCCGACTA GGAGATGGCG CCTCGGTAGC
235 G E C G A S S G M A D P N R F R G K D L A O
      ^end of light chain, start of gD tag

801 TGGCCCTAGT ACCCAAGTTC ACCTAAAAG GGTAACTAGA GGTGAGGTG ATTTATGAA AAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT
ACCGGGATCA TGCCTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAATACTT TTCTTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA
      M K K N I A F L L A S M F V F
      ^start of still

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901 TCTATTGCTA CAAACGGCTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG CAGCCAGGGG GCTCACTCCG TTTGTCTCTGT GCAGCTTCTG
AGATAACGAT GTTTGGCGAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCAC GTGGTCCCC CGAGTGAGGC AACACAGGACA CGTCGAAGAC
-8 S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S G
      ^start of heavy chain

1001 GCTTCACCAT TAGTGGTTCT TGGATACACT GGGTGGCTCA GGCCCGGGT AAGGCCTGG AATGGGTGC TTGGATTGCT CTTATAGCG GCGTACTGA
CGAAGTGGTA ATCACCAAGA ACCTATGTA CCCACGAGT CCGGGGCCA TTCCGGGACC TTACCCAACG AACCTAACGA GGAATATCG CCGCATGACT
27 F T I S G S W I H W V R Q A P G K G L E W V A W I A P Y S G A T D
      ^CDR-H2

1101 CTATGCCGAT AGCGTCAAGG GCCGTTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC
GATACGGCTA TCGCAGTTCC CGGCAAAGTG ATATTCCGGT CTGTGTAGGT TTTTGTGTCTG GATGGATGTT TACTTGTCTGA ATTCTCGACT CCTGTGACGG
60 Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T A

1201 GTCTATTATT GTCAAGAGA GGGGGGGCTTG TACTGGGTGT TCGACTACTG GGTCAAGGA ACACTAGTCA CCGTCTCTC GGCCTCCACC AAGGGCCCAT
CAGATAATAA CACGTTCTCT CCCCCCGAAC ATGACCCACA AGCTGATGAC CCCAGTTCCT TGTGATCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA
93 V Y Y C A R E G G L Y W V F D Y W G Q G T L V T V S S A S T K G P S
      ^CDR-H3

1301 CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT GCTTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG
GGCAGAAGG GGACCGTGGG AGGAGGTTCT CGTGGAGACC CCGGTGTCTG CCGGACCCGA CGGACCAAGT CCTGATGAAG GGGCTTGGCC ACTGCCACAG
127 V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V S

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FIG._27B

1401 GTGGAAC~~T~~CA GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGTGTCC TACAGTCCCTC AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC
 CACCTTGAGT CCGCGGGACT GGTGCGCGCA CGTGTGGAAG GGCCGACAGG ATGTCAGGAG TCCTGAGATG AGGAGTCGT CGCACCAC~~T~~G GCACGGGAGG
 160 W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S
 1501 AGCAGCTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG GTCGACAAGA AAGTTGAGCC CAATCTTGT GACAAAACTC
 TCGTCGAACC CGTGGGCTG GATGTAGACG TTGCACCTAG TGTTGGGTC GTTGTGGTTC CAGCTGTCT TTCAACTCGG GTTTAGAACA CTGTTT~~T~~GAG
 193 S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H
 1601 ACCTCAGTG CCGTGGCTCT GTTCCGGTG ATTTGATTA TGAAGAATG GCAAACGCTA ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGGCT
 TGGAGTCACC GCCACCGAGA CCAAGGCCAC TAAACTAAT ACTTTCTAC CGTTTGGAT TATCCCCCG ATACTGGCTT TTACGGCTAC TTTGCGCGGA
 227 L S G G S G S G D F D Y E K M A N A N K G A M T E N A D E N A L
 ^end of heavy chain
 ^start of gene III coat protein (267-end)
 1701 ACAGTCTGAC GCTAAAGGCA AACTTGATTC TGTCGCTACT GATTACGGTG CTGCTATCGA TGGTTTCATT GGTGACGTTT CCGGCTTGC TAATGGTAAT
 TGTGAGACTG CGATTTCCGT TTGAACTAAG ACAGCGATGA CTAATGCCAC GACGATAGCT ACCAAAGTAA CCAC~~T~~GCAAA GGCCGGAACG ATTACCATTA
 260 Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L A N G N
 1801 GGTGCTACTG GTGATTTGC TGGCTCTAAT TCCCAAATGG CTCAAGTCGG TGACGGTGAT AATCACCCTT TAATGAATAA TTTCCGTCAA TATTACCTT
 CCACGATGAC CACTAAACG ACCGAGATTA AGGTTTACC GAGTTCAGCC ACTGCCACTA TTAAGTGGAA ATTACTTATT AAAGCAGTT ATAATGGAA
 293 G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S
 1901 CCCTCCCTCA ATCGGTTGAA TGTGCGCCTT TTGCTTTTAG CGTGGTAA CCATATGAAT TTCTATTGA TTGTGACAAA ATAACTTAT TCCGTGGTGT
 GGGAGGGAGT TAGCCAACTT ACAGCGGGA AACAGAAATC GCACCACTT GGTATACCTA AAAGATAACT AACACCTTT TATTGAATA AGGCACCACA
 327 L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N L F R G V
 2001 CTTTGGCTT CTTTATATG TTGCCACCTT TATGTATGA TTTCTACGT TTGCTAACAT ACTGCGTAAT AAGAGTCTT AA
 GAAACGCAAA GAAATATAC AACGGTGGAA ATACATACAT AAAAGATGCA AACGATTGTA TGACGCTATA TTCTCAGAA TT
 360 F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG._27C

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1  ATGAAAAGA ATATCGCAT TCTTCTTCCA TCTATGTTCCG TTTTCTCTAT TGCTACAAAT GCCTATGCAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC
   TACTTTTCT TATAGCGTAA AGAAGACGT AGATACAAGC AAAAAGATA ACGATGTTTA CGGATACGTC TATAGGTCTA CTGGTCAGG GGCTCGAGGG
1M  K K N I A F L L A S M F V F S I A T N A Y A D I Q M T Q S P S S L
   ^met
   ^start of stII signal sequence

101 TGTCGGCTC TGTGGGGAT AGGTCACCA TCACCTGCCG TGCAGTCAG GATGTGTCCA CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAAGTCC
   ACAGGGGAG ACACCCGCTA TCCCAGTGGT AGTGACGGC ACGTCAGTC CTACACAGGT GACGACATCG GACCATAGTT GTCITTTGGTC CTTTTCGAGG
35  S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P
   ^CDR-L1

201 GAAGCTTCTG ATTTACTCG CATCCTTCTCT CTACTCTGGA GTCCTTCTC GCTTCTCTGG TAGCGGTTCC GGGACGGATT TCACCTCTGAC CATCAGCAGT
   CTTCGAAGAC TAAATGAGC GTAGGAAGCA GATGAGACCT CAGGAAGAG CGAAGAGACC ATCGCCAAGG CCCTGCCCTAA AGTGAGACTG GTAGTCGTC
68  K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S S
   ^CDR-L2

301 CTGCAGCGG AAGACTTCG AACTTATTAC TGTACCAAC ATTATACTAC TCCTCCACG TTCGGACAGG GTACCAAGT GGAGATCAAA CGAACTGTGG
   GACGTCGGC TTCTGAAGG TTGAATAATG ACAGTCGTTG TAAATGATG AGAGGGTGC AAGCCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC
101 L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T V A
   ^CDR-L3

401 CTGCACCATC TGTCTTCATC TTCCCGGCAT CTGATGAGCA GTTGAATCT GGAATGCCCT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC
   GACGTGGTAG ACAGAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA CTTGACGGA GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG
135  A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A

501 CAAAGTACAG TGAAGGTGG ATAACGCCCT CCAATCGGCT AACTCCCAGG AGAGTGTAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
   GTTTCATGTC ACCTTCCACC TATTGCGGA GGTGAGCCCA TTGAGGGTCC TCTCACAGTG TCTCGTCCCTG TCGTTCCCTGT CGTGGATGTC GGAGTCGTCG
168  K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGAGC TGAGCAAGC AGACTACGAG AAACACAAAG TCTACGCCCTG CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA
   TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATCGCGAC GCTTCAGTGG GTAGTCCCGG ACTCGAGCGG GCAGTGTTC TCGAAGTTGT
201 T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R

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FIG._28A

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701 GGGGAGAGTG TGGTCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAAGACC TGGCATAACT CGAGGCTGAT CCTCTAGCC GGACGCATCG
    CCCCTCTCAC ACCACGGTCG AGCCCATACC GACTAGGCTT GGCAAAGCGG CCATTCTCTGG ACCGTATTGA GCTCCGACTA GGAGATGGG CCTGCGTAGC
235 G E C G A S S G M A D P N R F R G K D L A O
    ^end of light chain, start of gD tag

801 TGGCCCTAGT ACCGAAGTTC ACCTAAAAG GGTAACTAGA GGTGAGGTG ATTTTATGAA AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT
    ACCGGGATCA TGGGTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAATACTTT TTCTTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAA
    M K K N I A F L L A S M F V F
    ^start of stII

-23

901 TCTATTGCTA CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG CAGCAGGGG GGTCACTCCG TTGTCTCTGT GCAGCTTCTG
    AGATAACGAT GTTGGGCAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCC GTCGGTCCCC CGAGTGAGGC AACACAGGACA CGTCGAAGAC
-8 S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S G
    ^start of heavy chain

1001 GCTTCACCAT TAGTAATTAT GGGATACACT GGGTGGCTCA GGGCCCGGGT AATGGGTGG TAGGATTCTT CCTTCTAACG GCTCTACTTA
    CGAAGTGGTA ATCATTATA CCTATGTGA CCCACGGAGT CCGGGGCCCA TTCCGGGACC TTACCCAAACC ATCCTAAAGA GGAAGATTGC CGAGATGAAT
27 F T I S N Y G I H W V R Q A P G K G L E W V G R I S P S N G S T Y
    ^CDR-H2

1101 CTATGCCGAT AGGTCGAAG GCGTTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC
    GATACGGCTA TCGAGTTCC CGGCAAAGTG ATATTCCGCT CTGTGTAGGT TTTTGTGTCTG GATGGATGTT TACTTGTCGA ATTCTCGACT CCTGTGACGG
60 Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T A

1201 GTCTATTATT GTCAAAATG CTCGGTCAGG TTCGCTTACT GGGGTCAAGG AACACTAGTC ACCGTCTCTT CGGCCTCCAC CAAGGGCCCA TCGGTCTTCC
    CAGATAATA CACGTTTTAC GAGCCAGTCC AAGCGAATGA CCCCAGTTCC TTGTGATCAG TGGCAGAGGA GCCGGAGGTG GTTCCCGGCT AGCCAGAAGG
93 V Y Y C A K C S V R F A Y W G Q G T L V T V S S A S T K G P S V F P
    ^CDR-H3

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FIG._28B

1301 CCCTGGCACC CTCCTCCAG AGCACTCTG GGGGCACAGC GGCCTGGG TGCCTGGTCA AGGACTACTT CCCCGAACCG GTGACGGTGT CGTGGAACTC
 GGGACCGTGG GAGGAGGTTT TCGTGGAGAC CCCCGTGTG CCGGACCCG ACGGACCACT TCCTGATGAA GGGGCTGGC CACTGCCACA GCACCTTGAG
 127 L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V S W N S
 1401 AGCGGCCCTG ACCAGCGGG TGCACACACTT CCCGGCTGTC CTACAGTCTC CAGGACTCTA CTCCTCAGC AGCGTGGA CCCTGCCCTC CAGCAGCTTG
 TCCGGGGAC TGGTCGGCG ACGTGTGGAA GGGCGGACAG GATGTCAGGA GTCCTGAGAT GAGGAGTCG TCGCACCACT GGCACGGGAG GTCGTCAAC
 160 G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S S S L
 1501 GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCACACCAA GGTGACAAG AAAGTTGAGC CCAATCTTG TGACAAAAC CACCTCAGT
 CCGTGGGTCT GGATGTAGAC GTTGCACTTA GTGTTCGGGT CGTTGTGGT CCAGCTGTTT CCAGCTGTC TTTCAACTCG GGTTTAGAAC ACTGTTTGA GTGAGTCA
 193 G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H L S G
 start of gene III coat protein (267-end)
 1601 GCGTGGCTC TGGTCCGGT GATTTTGATT ATGAAAAGAT GGCAACGCT AATAAGGGG CTATGACCGA AAATGCCGAT GAAAACGGC TACAGTCTGA
 CGCCACCGAG ACCAAGGCA CTAAACTAA TACTTTTCTA CCGTTTCCGA TTATTCCTCC GACTGGCT TTTACGGCTA CTTTGGCGG ATGTCAGACT
 227 G G S G S G D F D Y E K M A N A N K G A M T E N A D E N A L Q S D
 1701 CGCTAAAGC AACTTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCTTG CTAATGGTAA TGGTGTACT
 GCGATTCCG TTTGAACATA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAGTA ACCACTGCAA AGGCCGGAAC GATTACCAAT ACCACGATGA
 260 A K G K L D S V A T D Y G A A I D G F I G D V S G L A N G N G A T
 1801 GGTGATTTG CTGGCTCTAA TTCCCAATG GCTCAAGTCG GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA ATATTACCT TCCCTCCCTC
 CCACTAAAC GACCGAGATT AAGGTTTAC CAGTTTCAGC CACTGCCACT ATTAAGTGA AATTACTTAT TAAAGGCACT TATAAATGA AGGAGGGAG
 293 G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S L P Q
 1901 AATCGTTGA ATGTCGCCCT TTTGTCTTTA GCGTGGTAA ACCATATGAA TTTTCTATTG ATTGACAA AATAAACCTTA TTCCGTGGTG TCTTTGCCCT
 TTAGCCAACT TACAGCGGGA AACAGAAAT CCGGACCAAT TGGTATACTT AAAAGATAAC TAACACTGTT TTATTTGAT AAGGCACCAC AGAAACGCAA
 327 S V E C R P F V F S A G K P Y E F S I D C D K I N L F R G V F A F
 2001 TCTTTTATAT GTTCCACCT TTATGTATGT ATTTCTACG TTTGCTAACA TACTGCGTAA TAAGGAGTCT TAA
 AGAAATATA CACGGTGA AATACATACA TAAAGATGC AAACGATGT ATGACGCAAT ATTCCTCAGA ATT
 360 L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG.-28C

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1 ATGAAAAAGA ATATCGCATT TCCTCTTGCA TCCTATGTCG TTTTCTCTAT TGCTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCCGAGCT
TACTTTTTCT TATAGCGTAA AGAAGACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S
^met
^start of stII signal sequence
^light chain start

101 CCCTGTCCGC CTCTGTGGC GATAGGCTCA CCATCACCTG CCCTGCCAGT CAGGATGTGT CCACTGCTGT AGCCTGSPAT CAACAGAAAC CAGGAAAAAGC
GGGACAGGCG GAGACACCGG CTATCCAGT GGTAGTGGAC GGCACGGTCA GTCTACACA GGTGACGACA TCGGACCATA GTTGTCTTGT GTCTTTTCG
35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A
^CDR-L1

201 TCCGAAGCTT CTGATTACT CGGATTCCTT CCTCTACTCT GAGTCCCTT CTGGCTTCTC TGGTAGCGGT TCCGGGACGG ATTTCACTCT GACCATCAGC
AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCCG
68 P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S
^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTCTCAGC AATCTTATAC TACTCTCCCTCC AGGTTCGGAC AGGTTACCAA GGTGGAGATC AAACGAAGTC
TCAGACGTCG GCCTTCTGAA CGGTTGATA ATGACAGTCG TTAGAATATG ATGAGGAGGG TGCAAGCCTG TCCCATGTTT CCACCTCTAG TTTTGTGTGAC
101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V
^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCGC CATCTGATGA GCAGTTGAAA TCTGGAAC TGCTGTGTGT GTGCTGTGTG AATACTTCT ATCCAGAGA
ACCGACGTGG TAGACAGAG TAGAAGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGCTCTCT
135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGGAGG TGGATAACGC CCTCCAATCG GGTAACTCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
CCGGTTTCTAT GTCACCTTCC ACCTATTGCG GGAGTTAGC CCATGAGGG TCCTCTCACA GTGTCTCGTC CTGTCTGTTCC TGTCGTGGAT GTCCGAGTCCG
168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGTCC GCCCGTCACA AAGAGCTTCA
TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCCTTGTGT TTGAGATCG GAGCTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

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FIG._29A

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701 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CGGGTAAGG ACCTGGCAFA ACTCGAGGCT GATCCTCTAC GCCGGACGCA
    TGTCCCTCTT CACACCACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAG GGGCCATTCC TGGACCGTAT TGAGCTCGA CTAGGAGATG CGGCCTGCGT
235 R G E C G A S S G M A D P N R F R G K D L A O
    ^end of light chain, start of gD tag

801 TCGTGGCCCT AGTACGGCAG TTCACGTAAG AAGGTAACCT AGAGTTGAG GTGATTTTAT GAAAAAGAAAT ATCGCATTC TTTCTGCATC TATGTTTCGT
    AGCACCGGGA TCATGCCGTTT AAGTGCATTT TTCCCATTTA TCTCCAACTC CACTAAAATA CTTTTTCTTA TAGCGTAAG AAGAACGTAG ATACAAGCAA
    M K K N I A F L L A S M F V
-23 ^start of stII

901 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CCGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT
    AAAAGATAAC GATGTTTGGG CATGCCACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTCGGTC CCCCAGATGA GGCAACACAGG ACACGTCGAA
-9 F S I A T N A Y A E V Q L V E S G G G L V Q P G S L R L S C A A S
    ^start of heavy chain ^CDR-H1

1001 CTGGCTTAC CATTAGTGGT TCTGATATAC ACTGGTGCG TCAGGCCCGG GGTAAAGGCC TGAATGGGT TGGTAGGATT TCTCCTTATG GCGCAATAC
    GACCGAAGTG GTAATCACCA AGACTATATG TGACCCACGC AGTCGGGGC CCATTCCCG ACCTTACCCA ACCATCTTAA AGAGGAATAC CGCCGTTATG
26 G F T I S G S D I H W V R Q A P G K G L E W V G R I S P Y G N T
    ^CDR-H2

1101 TAACTATGCC GATAGCGTCA AGGCCCGTTT CACTATAAGC GCACACACAT CCAAAAACAC AGCCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
    ATTGATACGG CTATCGCAGT TCCCGGCRAA GTGATATTCTG CGTCTGTGTA GGTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCTCG ACTCCTGTGA
59 N Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T

1201 GCGTCTATT ATTGTGCAAG AGTCGGCGGC CTCAAGTTGC TGTTCGACTA CTGGGGTCAA GGAACACTAG TCACCGTCTC CTCGGCCTCC ACCAAGGGCC
    CGGCAGATAA TAACACGTTT TCAGCCCGCG GAGTTCAACG ACAAGCTGAT GACCCCAAGT CTTGTGATC AGTGGCAGAG GAGCCGGAGG TGGTTCCCGG
92 A V Y Y C A R V G G L K L L F D Y W G Q G T L V T V S S A S T K G P
    ^CDR-H3

1301 CATCGGTCTT CCCCCTGGCA CCTCTCTCCA AGAGCACCTC TGGGGGCACA GGGGCCCTGG GCTGCCTGGT CAAGGACTAC TTCCCCGAAC CGGTGACGGT
    GTAGCCAGAA GGGGGACCGT GGGAGGAGT TCTCGTGGAG ACCCCGCTGT CCGCGGGACC CGACGGACCA GTTCTGTATG AAGGGGCTTG GCCACTGCCA
126 S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V

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FIG._29B

1401 GTCGTGAAC TCAGGCGCCC TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACCGTGCCC
 CAGCACCTTG AGTCGCGGGG ACTGGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTGAG GAGTCCTGAG ATGAGGAGT CGTGCACCA CTGGCACGGG
 159 S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P
 1501 TCCAGCAGCT TGGGCACCCA GACCTACATC TGAACGTGA ATCACAAGCC CAGCAACACC AAGGTCGACA AGAAGTTGA GCCCAAATCT TGTGACAAAA
 AGGTGCTCGA ACCCGTGGGT CTGGATGTAG ACCTTGCACT TAGTGTTCGG GTCGTTGTTGG TTCCAGTGT TCTTTCAACT CGGTTTGA ACACGTGTTT
 192 S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T
 1601 CTCACGGCGG CATGAACAG CTAGAGGACA AGTCGAAGA GCTACTCTCC AAGAACTACC ACCTAGAGAA TGAAGTGGCA AGACTCAAAA AACTGTGCGG
 GAGTGCCGGC GTACTTGTGTC GATCTCTGT TCCAGCTTCT CGATGAGAGG TTCTTGATGG TGGATCTCTT ACCTCACCGT TCTGAGTTT TTGAACAGCC
 226 H G R M K Q L E D K V E E L L S K N Y H L E N E V A R L K K L V G
 *end of heavy chain, start of leucine zipper
 1701 GGAGCGCGG AAGCTTAGTG CGGTGGCTC TGTTCCGGT GATTTTGATT ATGAAAAGAT GGCAACGCT AATAAGGGG CTATGACCGA AAATGCCGAT
 CCTCGCGCCT TTCGATCAC CGCCACCGAG ACCAAGGCCA CTAAACTAA TACTTTTCTA CCGTTTCCGA TTATTTCCCC GATACTGGCT TTACGGCTA
 259 E R G K L S G G S G D F D Y E K M A N A N K G A M T E N A D
 *end of leucine zipper, gene III coat protein (267-end)
 1801 GAAAACGGC TACAGTCTGA CGCTAAAGGC AAACCTTGATT CTGTGCTAC TGATTACGGT GCTGCTATCG ATGTTTTCAT TGGTGACGTT TCCGGCCTTG
 CTTTTCGGG ATGTCAGACT GCGATTTCG TTTGAACTAA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAAGTA ACCACTGCAA AGGCCGGAAC
 292 E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L A
 1901 CTAATGCTAA TGGTGCTACT GGTGATTTTG CTGCTCTAA TTCCCAAATG GCTCAAGTCG GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA
 GATTACCAT ACCACGATGA CCACATAAAC GACCGAGATT AAGGTTTAC CGAGTTCAGC CACTGCCACT ATTAAGTGA AATTAATTAT TAAAGGCAGT
 326 N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q
 2001 ATATTACCT TCCCTCCCTC AATCGGTTGA ATGTCGCCCT TTGTCTTTA GCGTGGTAA ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACTTA
 TATAAATGA AGGAGGGAG TTAGCCAAC TACAGCGGA AACAGAAAT CGCGACCAAT TGGTATACCT AAAAGATAAC TAACACTGTT TTATTTGAAT
 359 Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N L
 2101 TTCGGTGGT TCTTTGCGTT TCTTTTATAT GTTGCACCT TTATGTATGT ATTTTCTACG TTGCTAACA TACTGCTAA TAAGGAGTCT TAA
 AAGGCACCAC AGAAACGCA AGAAATATA CAACGGTGA AATACATACA TAAAGATGC AAACGATTGT ATGACGATT ATTCCTCAGA ATT
 392 F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG._29C


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1 ATGAAAAGA ATATCGCATT TCTTCTTGA TCTATGTTG TTTTCTTCTAT TGCTACAAAT GCCTATGCAAT CCGATATCCA GATGACCCAG TCCCCGAGCT
TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S
^start of stII signal sequence
^met
^light chain start

101 CCCTGTCCGC CTCTGTGGC GATAGGGTCA CCATCACCTG CCGTGCCAGT CAGGATGTGT CCACTGCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
GGGACAGGGC GAGACACCCG CTATCCCACT GGTAGTGGAC GGCACGGTCA GTCCTACACA GTGACGACA TCGGACCATA GTTGCTTTTG GTCCTTTTCG
35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A
^CDR-L1

201 TCCGAAGCTT CTGATTACT CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTCGCTTCTC TGGTAGCGGT TCCGGGACGG ATTTCACTCT GACCATCAGC
AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG
68 P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S
^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTGAGC AATCTTATAC TACTCTCTCC ACCTTCGGAC AGGTACCAA GGTGGAGATC AAACGAACTG
TCAGACGTCG GCCTTCTGAA CGGTTGAATA ATGACAGTCG TTAGATATAG ATGAGGAGGG TCGAAGCCTG TCCCATGGTT CCACCTCTAG TTTGCTTGAC
101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V
^CDR-L3

401 TGCTGCACC ATCTGTCTC ATCTTCCGC CATCTGATGA GCAGTTGAAA TCTGGAACCTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGGTCTCT
135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGAAGG TGGATAACGC CCTCCAAATCG GGTAACTCCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
CCGGTTTCAT GTCACCTTCC ACCTATTGGG GGAGGTTAGC CCATTGAGGG TCCTCTCACA GTGTCTCGTC CTGTCTGTCC TGTCGTGGAT GTCGGAGTCG
168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
TCGTGGGACT CGGACTCGTT TCGTCTGATG CTCCTTTGTT GTTCAATGCG GACGTTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

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FIG._30A

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701 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACGGTTTC CGCGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCGGAGCGCA
TGTCCCTCT CACACCACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAAG GCGCATTC GCGCATTC TGAGCTCCGA CTAGGAGATG CCGCCTGCGT
235 R G E C G A S S G M A D P N R F R G K D L A O
^end of light chain, start of gD tag

801 TCGTGGCCCT AGTACGCAAG TTCACGTAAA AAGGTAAC AGAGGTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTC TTCTTGCATC TATGTTGTT
AGCACCGGA TCATGCGTTC AAGTGCATTT TTCCCATTTGA TCTCCAATC CACTAAAATA CTTTTCCTTA TAGCGTAAAG AAGAACCTAG ATACAGCAA
-23 M K K N I A F L L A S M F V
^start of stII

901 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGTGG TGGAGTCTGG CCGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT
AAAAGATAAC GATGTTTGG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTCGGTC CCCCGAGTGA GGCAACAGG ACACGTCGAA
-9 F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S
^start of heavy chain ^CDR-H1

1001 CTGGCTTCAC CATTACTAAT TCCGATATAC ACTGGGTGCG TCAGGCCCGG GGTAAAGGCC TGGAATGGGT TGCTACTATT TATCCTTTATG GCGGCTATAC
GACCGAAGTG GTAATGATTA AGGCTATATG TGACCCACGC AGTCGGGGC CCATTCCCGG ACCTTACCCA ACATGATATA ATAGGATATC CGCCGATATG
26 G F T I T N S D I H W V R Q A P G K G L E W V A T I Y P Y G G Y T
^CDR-H2

1101 TTACTATGCC GATAGCGTCA AGGGCCGTTT CACTATAAGC GCAGACACAT CCAAAAACAC AGCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
AATGATACGG CTATCGCAGT TCCCGGCCAA GTGATATTCG CGTCTGTGTA GGTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCCTG ACTCCTGTGA
59 Y Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T

1201 GCGGCTTATT ATTGTGCAAG AGGGGGCGGG ATGGACGGCT ACGTTATGGA CTACTGGGGT CAAGGAACAC TAGTCACCGT CTCCTCGGCC TCCACCAAGG
CGGCAGATAA TAACACGTTT TCCCCCGCCC TACCTGCCGA TGCATACCT GATGACCCCA GTTCCTTGTG ATCAGTGGCA GAGGAGCGG AGGTGTTCC
92 A V Y Y C A R G G G M D G Y V M D Y W G Q G T L V T V S S A S T K G
^CDR-H3

1301 GCCCATCGGT CTTCCCCCTG GCACCTCTCT CCAAGAGCAC CTCTGGGGG ACAGCGGCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC
CGGGTAGCCA GAAGGGGGAC CGTGGGAGGA GGTTCCTGTG GAGACCCCGG TGTGCGCCGG ACCCGACGGA CCAGTTCCTG ATGAAGGGC TTGGCCACTG
126 P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T

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FIG._30B

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1401 GGTGTCGTGG AACTCAGCG CGCGGTGCAC ACCTTCCCG CTGTCTCTACA GTCTACTCCC TCAGCAGCGT GGTGACCGTG
    CCACAGCACC TTGAGTCCGC GGGACTGGTC GCCGCACGTG TGAAGGGCC GACAGGATGT CAGGAGTCTT GAGATGAGGG AGTCGTCGCA CCACTGGCAC
159 V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V

1501 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGCTCG ACAAGAAAGT TGAGCCCAA TCTTGTGACA
    GGGAGGTCGT CGAACCCGTG GGTCTGGATG TAGACGTTGC ACTTAGTGT CCGGTCTGTG TGGTTCAGC TGTTCTTTCA ACTCGGGTTT AGAACACTGT
192 P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K

1601 AACTCAGCG CCGCATGAAA CAGCTAGAGG ACAAGGTGCA AGAGTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAACTTGT
    TTTGAGTGCC GGGGTACTTT GTCGATCTCC TGTTCAGCT TCTCGATGAG AGGTTCTTGA TGGTGGATCT CTTACTTCAC CGTTCTGAGT TTTTGAACA
226 T H G R M K Q L E D K V E E L L S K N Y H L E N E V A R L K K L V
    ^end of heavy chain, start of leucine zipper

1701 CGGGGAGCGC GGAAGCTTA GTGGGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAA GATGGCAAC GCTAATAAGG GGGCTATGAC CGAAAAATGCC
    GCCCCTCGCG CCTTTCGAAT CACCGCCACC GAGACCAAGG CCACATAAAC TAATACTTTT CTACCGTTTG CGATTATTCC CCGATACTG GCTTTTACGG
259 G E R G K L S G G S G S G D F D Y E K M A N A N K G A M T E N A
    ^end of leucine zipper, start of gene III coat protein (267-end)

1801 GATGAAAACG CGCTACAGTC TGACGCTAAA GCGAAACTTG ATTCTGTGCG TACTGATTAC GGTGCTGCTA TCGATGGTTT CATTTGGTAC GTTCCGGCC
    CTACTTTTGC GCGATGTCAG ACTGGGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAA GTAACCACTG CAAAGGCCGG
292 D E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L

1901 TTGCTAATGG TAATGGTGCT ACTGGTGATT TTGCTGGCTC TAATTCCTCA ATGGCTCAAG TCGGTGACGG TGATAATTCA CCTTAATGA ATAATTCCG
    AACGATTACC ATTACCACGA TGACCACCTAA AACGACCGAG ATTAAGGTTT TACCGAGTTC AGCCACTGCC ACTATTAAAGT GGAATTAAT TATTAAAGGC
326 A N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R

2001 TCAATATTTA CCTTCCCTCC CTCATTCGGT TGAATGTGCG CCTTTTGTCT TTAGCGCTGG TAAACCATAT GAATTTTCTA TTGATTGTGA CAAATAAAC
    AGTTATAAAT GGAAGGAGG GAGTTAGCCA ACTTACAGCG GGAACACAGA AATCGCGACC ATTTGGTATA CTTAAAGAT AACTAACACT GTTTATTTG
359 Q Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N

2101 TTATTCCTGT GTGTCCTTTC GTTTCTTTTA TARGTTGCCA CCTTTATGTA TGTATTTTCT ACGTTTGTCTA ACATCTGCG TAATAAGGAG TCTTAA
    AATAAGGCAC CACAGAAACG CAAAGAAAAT ATACAAACGT GGAATATCAT ACATAAAGA TGCAAAAGAT TGTATGACGC ATTATTCCTC AGAATT
392 L F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

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FIG._30C

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1 ATGAAAAAGA ATATCGCAFT TCTTCTTGCA TCTATGTCG TTTTCTCTAT TGCTACAAAT GCCTATGCAAT CCGATATCCA GATGACCCAG TCCCCGAGCT
TACTTTTTCT TATAGCGTAA AGAAGAAGC AGATAACAAGC AAAAAGATA ACGATGTTTA CGGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S
^met ^light chain start

101 CCCTGTCCGC CTCTGTGGC GATAGGGTCA CCATCACCTG CCGTCCAGT CAGATGTGT CCACTGCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
GGGACAGGGG GAGACACCCG CTATCCAGT GGTAGTGGAC GGCACGGTCA GTCTACACA GGTGACGACA TCGGACCATA GTTGTCTTTG GTCCTTTTCG
35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A
^CDR-L1

201 TCCGAAGCTT CTGATTACT CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTGCTTCTC TGGTAGCGGT TCCGGGACGG ATTTCACCTCT GACCATCAGC
AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG
68 P K L L I Y S A S F L Y S G V P S R F S G S G T D F T L T I S
^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTGAGC AATCTTATAC TACTCCTCCC ACGTTCCGAC AGGTACCRAA GGTGGAGATC AAACGAACTG
TCAGACGTCG GCCTTCTGAA CGGTTGAATA ATGACACTCG TTAGATATG ATGAGGAGG TGAAGCCTG TCCCATGGTT CCACCTCTAG TTTGCTTGAC
101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V
^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCGC CATCTGATGA GCAGTTGAAA TCTGGAAGTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
ACCGACGTCG TAGACAGAAG TAGAAGGGG GTAGACTACT CGTCACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGTCCTCT
135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAAGTA CAGTGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
CCGGTTTCAT GTCACCTTCC ACCTATTGGG GGAGGTTAGC CCATTGAGG TCTCTCACA GTGTCTCGTC CTGTCTGTTCC TGTCGTGGAT GTCGGAGTCG
168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTTGTGT TTCAGATCGG GACGTTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

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FIG._31A

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701 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CCGGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA
    TGTCCCTCTT CACACCACGG TCGAGGCCAT ACCGACTAGG CTTCGGCAAAG GGCCTATTCC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CGGCCCTGCGT
235 R G E C G A S S G M A D P N R F R G K D L A O
    ^end of light chain, start of gD tag

801 TCGTGGCCCT AGTACGCAAG TTCACGTAAA AAGGTAACCT AGAGTTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTT TTCTTGCAATC TATGTTGCTT
    AGCACCGGGA TCATGGGTTT AAGTGCATTT TTCCCATTTGA TCCTCAACTC CACTAAATA CTTTTCTTA TAGCGTAAAG AAGAACCTAG ATACAGCAA
    M K K N I A F L L A S M F V
-23 ^start of stII

901 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CCGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT
    AAAAGATAAC GATGTTTGG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTGGTC CCCCGAGTGA GGCAACAGG ACACGTGCGAA
-9 F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R L S C A A S
    ^start of heavy chain

1001 CTGGCTTCAC CATTATAAT TATGATATAC ACTGGTGGCG TCAGGCCCGG GGTAAAGGCC TGAATGGGT TGGTTATATT TCTCTCTTA CGGGCGCTAC
    GACCGAAGTG GTAATTATTA ATACTATATG TGACCCACGC AGTCGGGGC CCATTCCCG ACCTTACCCA ACCAATATAA AGAGGAGGAT CGCCGGGATG
26 G F T I N N Y D I H W V R Q A P G K G L E W V G Y I S P P S G A T
    ^CDR-H2

1101 TTTACTATGCC GATAGCGTCA AGGGCCGTTT CACTATAAGC GCAGACACAT CCAAAAACAC AGCTTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
    AATGATACGG CTATCGCAGT TCCCGGCAAA GTGATATTGG CGTCTGTGTA GGTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCCTG ACTCCTCTGA
59 Y Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T

1201 GCCGTCTATT ATTGTGCAAG AATGGTCGGC ATGGCGAGGG GGGTTATGGA CTACTGGGGT CAAGGAACAC TAGTCACCGT CTCCTCGGCC TCCACCAAGG
    CGGCAGATAA TAACACGTTT TTACCAGCGG TACGCCCTCC CCCAATACCT GATGACCCCA GTTCCTTGTG ATCAGTGGCA GAGGAGCCGG AGGTGGTTCC
92 A V Y Y C A R M V G M R R G V M D Y W G Q G T L V T V S S A S T K G
    ^CDR-H3

1301 GCCCATCGGT CTTCCTCCCTG GCACCTCTCT CCAAGAGCAC CTCTGGGGG ACAGCGGCC TGGGCTGCCT GGTCAAGGAC TACTTCCCG AACCGGTGAC
    CGGGTAGCCA GAAGGGGGAC CGTGGGAGGA GGTTCTCTGT GAGACCCCGG TGTCGCCCGG ACCCGACGGA CCAGTTCTCTG ATGAAGGGGC TTGGCCACTG
126 P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T

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FIG._31B

1401 GGTGTCGTGG AACTCAGCGG CCCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCCTACA GTCTACTCCC TCACAGCGT GGTGACCGTG
 CCACAGCACC TTGAGTCCGC GGGACTGGTC GCGGCACGTG TGAAGGGCC GACAGGATGT CAGGAGTCTT CAGATGAGGG AGTCGTCCGA CCACTGGCAC
 159 V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V
 1501 CCCTCCACCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGTTCG ACAAGAAAGT TGAGCCCAAA TCTTGTGACA
 GGGAGGTGGT CGAACCCGTG GGTCTGGATG TAGACGTTGC ACTTAGTGTT CGGGTCGTTG TGGTTCAGC TGTTCCTTCA ACTCGGGTTT AGAACACTGT
 192 P S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K
 1601 AAACCTCAGG CCGCATGAAA CAGCTAGAGG ACAAGGTGCA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAATTGT
 TTTGAGTGCC GCGGTACTTT GTCGATCTCC TGTTCAGCT TCTCGATGAG AGGTTCTTGA TGGTGGATCT CTTACTTCAC CGTCTGAGT TTTTGAACA
 226 T H G R M K Q L E D K V E E L L S K N Y H L E N E V A R L K K L V
 ^end of heavy chain, start of leucine zipper
 1701 CGGGGAGCGG GGAAGCTTA GTGGCGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAA GATGGCAAC GCTAATAAGG GGGCTATGAC CGAATAATGCC
 GCCCTCGGG CCTTTCGAAT CACCGCCACC GAGACCAAGG CCACATAAAC TAATACTTTT CTACCGTTTG CGATTATTC CCGGATCTG GCTTTACGG
 259 G E R G K L S G G S G D F D Y E K M A N A N K G A M T E N A
 ^end of leucine zipper
 ^gene III coat protein (267-end)
 1801 GATGAAAACG CGCTACACTC TGACGCTAAA GGCAAACTTG ATTCTGTCG TACTGATTAC GGTGCTGCTA TCGATGGTTT CATTTGCTGAC GTTTCGGGCC
 CTACTTTTGC GCGATGTCAG ACTGGGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAAA GTAACCACTG CAAAGSCCGG
 292 D E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L
 1901 TTGCTAATGG TAATGGTGCT ACTGGTGATT TTGCTGGCTC TAATTCCTAA ATGGCTCAAG TCGGTGACGG TGATAAATCA CCTTTAATGA ATAAATTTCCG
 AACGATTACC ATTACCACGA TGACCCTAA AACGACCGAG ATTAAGGGTT TACCGAGTTC AGCCACTGCC ACTATTAACT GGAATTAAGT TATTAAAGGC
 326 A N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R
 2001 TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTCG CCTTTTGTCT TTAGCGCTGG TAAACCATAT GAATTTTCTA TTGATTTGTA CAAATAAAC
 AGTTATAAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGCG GGAACACAGA AATCGCGACC ATTTGGTATA CTTAAAGAT AACTAACACT GTTTTATTG
 359 Q Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N
 2101 TTATTCGGTG GTGTCCTTTG GTTCTTTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACGTTTGCTA ACATACGCG TAATAAGGAG TCTTAA
 AATAAGGCAC CACAGAAACG CAAAGAAAT ATACAACGGT GGAATACAT ACATAAAGA TGCAACGAT TGTATGACG ATTATCTCTC AGAATT
 392 L F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG._31C

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1 GAATTCAACT TCCTCATACT TTGGATAAGG AAATACAGAC ATGAAAATC TCATTGCTGA GTTCTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
  CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGCTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTTCGACGGG TTTTCTTCTT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACACGG GTTGATTGAT CAGGTAGAGG
  CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CCGCTTTTAC TGGTGTGCGC CAACTAACTA GTCCATCTCC

201 GGGCGGTGTA CGAGGTAAAG CCGATGCCA GCATTCCCTGA CGACGATAGG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
  CCGCGGACAT GCTCCATTTC GGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCACAA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTATTT TTTTAAATGTA TTGTAACTA GTACGCAAGT
  TTTTCAATTA GAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATGTA GAGGTGAGG TGATTTTATG AAAAGAATA TCGCATTTCT TCTTCGATCT ATGTCGTTT TTTCTATTGC TACAAATGCC
  AGTGCATTTT TCCCAACTCC ACTAAATAC TTTTCTTAT AGCGTAAAGA AGAAGTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG
  0 M K K N I A F L L A S M F V F S I A T N A
    ^start of stII signal sequence

501 TATGCAGATA TCCAGATGAC CCAGTCCCCG AGCTCCCTGT CCGCTCTGT GGGCGATAGG GTCACCATCA CCTGCGTGC CAGTCAGGAT GTGTCCACTG
  ATACGCTTAT AGGCTACTG GGTGAGGGC TCGAGGGACA GCGGGAGACA CCCGCTATCC CAGTGGTAGT GGACGGCAGC GTCAGTCCTA CACAGGTGAC
  21 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T A
    ^start of light chain
    ^CDR-L1
    ^EcoRV

601 CTGTAGCTG GTATCAACAG AAACCAGGAA AAGCTCCGAA GCTTCTGATT TACTCGGCAT CCTTCCTCTA CTCTGGAGTC CCTTCTCGT TCTCTGGTAG
  GACATCGGAC CATAGTTGTC TTTGGTCCCTT TTCGAGGCTT CGAAGACTAA ATGAGCCGTA GGAAGGAGAT GAGACCTCAG GGAAGAGCGA AGAGACCATC
  55 V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S
    ^CDR-L2

701 CGGTTCCGGG ACGGATTTCA CTCTGACCAT CAGCAGTCTG CAGCCGGAAG ACTTCGCAAC TTATTACTGT CAGCAATCTT ATACTACTCC TCCCACGTTT
  GCCAAGGGCC TGCCCTAAAGT GAGACTGGTA GTGCTCAGAC GTCGGCCTTC TGAAGCGTTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGTTGCAAG
  88 G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F
    ^CDR-L3

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FIG._32A

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801 GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGCTG CACCATCTGT CTTCATCTTC CCGCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCTCTG
    CCTGTCCCAT GGTTCACCT CTAGTTTGCT TGACACCCGAC GTGGTAGACA GAAGTAGAAG GCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGGAGAC
121 G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V
    ^KpnI

901 TTGTGTGCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACACTGG AAGGTGGATA ACSCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTCACAGA
    AACACACGGA CGACTTATTG AAGATAGGGT CTCTCCGGTT TCATGTCACC TTCCACCTAT TCGGGGAGGT TAGCCCATG AGGTCCTCT CACAGTGTCT
155 V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E

1001 GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAAGCAGA CTAGAGAAA CACAAAGTCT ACGCCTGCGA AGTCACCCAT
    CGTCTGTGCG TTCTGTGCTG GATGTGCGA GTCGTGCTGG GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TCGGACGCT TCAGTGGGTA
188 Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H

1101 CAGGGCCTGA GCTGCCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTCGCGGT AAGGACCTGG
    GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCCC CTCTCACACC ACGGTGAGG CCATACCGAC TAGGCTTGGC AAAGCGGCCA TTCCTGGACC
221 Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L A
    ^end of light chain, start of gD tag

1201 CATAACTCGA GGTGATCCT CTACGCCGGA CGCATCGTGG CCTAGTACG CAAGTTCACG TAAAGAGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA
    GTATTGAGCT CCGACTAGGA GATGCGGCCT GCGTAGCACC GGGATCATGC GTTCAAGTGC ATTTTCCCA TTGATCTCCA ACTCCACTAA AATACTTTTT
255 O
    M K K
    ^start of stII

-23
    ^start of heavy chain
    ^BsiWI

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FIG._32B

1401 CCAGGGGGCT CACTCCGTTT GTCTGTGCA GCTTCTGGCT TCACCATAG TGGTTCTTGG ATACACTGGG TGGTCAAGC CCGGGTAAG GGCCTGGAAT
 GGTCCCCCGA GTGAGGCAG CAGGACAGT CGAAGACCGA AGTGGTAATC ACCAAGAACC TATGTGACCC ACGCAGTCCG GGGCCCATTC CCGGACCTTA
 14 P G G S L R L S C A A S G F T I S G S W I H W V R Q A P G K G L E W
 ^CDR-H1
 1501 GGGTTGCTTG GATTGCTCCT TATAGCGCG CTACTGACTA TGCGGATAGC GTCAAGGGCC GTTTCACATAT AAGCGCAGAC ACATCCAAAA ACACAGCCTA
 CCCAACGAACTAAG CTAACGAGGA ATATCGCGCG GATGACTGAT ACGCTATCG CAGTTCCCGG CAAAGTGATA TTCCGGTCTG TGTAGGTTTT TGTGTCGGAT
 48 V A W I A P Y S G A T D Y A D S V K G R F T I S A D T S K N T A Y
 ^CDR-H2
 1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATATATTG CAAGAGAGGG GGGCTTGATC TGGTGTTCCG ACTACTGGG TCAAGGAACA
 GGATGTTTAC TTGTGGAATT CTCGACTCCT GTGACGGCAG ATATAACAC GTTCTCTCCC CCCGAACATG ACCCACAAGC TGATGACCCC AGTTCCCTGT
 81 L Q M N S L R A E D T A V Y Y C A R E G G L Y W V F D Y W G Q G T
 ^CDR-H3
 1701 CTAGTCACCG TCTCCTCCGC CTCCACCAAG GGGCCATCGG TCTTCCCCCT GGCACCTCC TCCAAGAGCA CCTCTGGGG CACAGCGGCC CTGGGCTGCC
 GATCAGTGGC AGAGGAGCG GAGGTGTTTC CCGGTAGGCC AGAGGGGGA CCGTGGGAGG AGGTTCTCGT GGAGACCCCC GTGTGCGCGG GACCCGACGG
 114 L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C L
 ^ApaI
 1801 TGGTCAAGGA CTACTTCCCC GAACCGGTGA CGGTGTGCTG GAACCTAGGC GGCCTGACCA GCGGCGTGCA CACCTTCCC GCTGTCTTAC AGTCTCAGG
 ACCAGTTCTT GATGAAGGG CTTGGCCACT GCCACAGCAC CTTGAGTCCG CGGACTGGT CCGCGCACGT GTGGAAGGCG CGACAGGATG TCAGGAGTCC
 148 V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G
 1901 ACTCTACTCC CTCAGCAGG TGGTGACCGT GCCCTCCAGC AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA CACCAAGGTC
 TGAGATGAGG GAGTCGTCCG ACCACTGSCA CCGGAGGTG TCGAACCCGT GGTCTTGGAT GTAGACGTTG CACTTAGTGT TCGGTCTGTT GTGGTTCCAG
 181 L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V
 2001 GACAAGAAAG TTGAGCCCCA ATCTTGTGAC AAAACTCACC TCTAGAGTGG CGGTGGCTCT GGTTCGGGTG ATGCTCGGTT GCCGCCGGGC GTTTTTATG
 CTGTTCTTTC AACTCGGTT TAGAACACTG TTTTGTAGTGG AGATCTCACC GCCACCGAGA CCAAGGCCAC TACGAGCCAA CCGCGGCCCG CAAAAAATAC
 214 D K K V E P K S C D K T H L O
 2101 CTAGCGCGCG CCTATACCTT GTCTGCCCTC CCGGTTGCG TCGCGGTGCA TGGAGCCGGG CCACCTCGAC CTGAATGGA GCCGGCGGCA CCTCGCTAAC
 GATCGCGGCG GGATATGGAA CAGACGGAGG GCGGCAACGC AGCGCCACGT ACCTCGGCCC GTTGGAGCTG GACTTACCTT CCGCGGCCCT GGAGCGATTG

FIG._32C

2201 GGATTACCA CTCAAGAAT TGGAGCCAAT CAATTCCTTGC GGAGAACTGT GAATGCGCAA ACCAACCCTT GGCAGAACAT ATCCATCGCG TCCGCCATCT
CCTAAGTGGT GAGTTCTTAA ACCTCGGTTA GTTAAGAAG CCTCTTGACA CTTACGCGTT TGGTTGGGAA CCTCTTGTA TAGGTAGCG AGCGGTTAGA

2301 CCAGCAGCCG CACCGGGCG ATCTCGGGCA GCGTTGGGTC CTGGCCACGG GTGGCGATGA TCGTCTCCT GTCTTGAGG ACCCGGCTAG GCTGGCGGGG
GGTCGTCGGC GTGCGCCGG TAGAGCCCGT CGCAACCCAG GACCGGTGCC CACGCGTACT AGCAGGAGGA CAGCAACTCC TGGGCGGATC CGACCGCCCC

2401 TTGCCCTTACT GGTAGCAGA ATGAATCACC GATACGGGAG CGAACGTGAA GCGACTGCTG CTGCAAAAACG TCTGCGACCT GAGCAACAAC ATGAATGGTC
AACGGAATGA CCAATCGTCT TACTTAGTGG CTATGCGCTC GCTTGCACTT CGCTGACGAC GACGTTTTC AGACGCTGGA CTCGTTGTTG TACTTACCAG

2501 TTCCGTTTCC GTGTTTCGTA AAGTCTGGAA ACGCGGAAGT CAGCGCCCTG CACCATATATG TTCCGGATCT GCATCGCAGG ATGCTGCTGG CTACCCCTGTG
AAGCCAAAGG CACAAAGCAT TTCAGACCTT TCGGCCCTTCA GTCGCGGGAC GTGGTAATAC AAGCCTAGA CGTAGCGTCC TAGCAGACC GATGGGACAC

2601 GAACACCTAC ATCTGTATTA ACGAAGCGCT GGCATTGACC CTGAGTGATTT TTCTCTGCTT CCGCGCGCAT CCATACCGCC AGTTGTTTAC CCTCACAACG
CTTGTTGATG TAGACATAAT TGCTTCGGA CCGTAACTGG GACTCACTAA AAGAGACCA GGGCGGCGTA GGTATGGCGG TCAACAAATG GGAGTGTTCG

2701 TTCCAGTAAC CGGCGATGTT CATCATCAGT AACCGTATC GTGAGCATCC TCTCTCGTTT CATCGTATC ATTACCCCCA TGAACAGAAA TTCCCCCTTA
AAGTTCATTG GCCCGTACAA GTAGTAGTCA TTGGGCATAG CACTCGTAGG AGAGAGCAA GTAGCCATAG TAATGGGGT ACTGTCTTT AAGGGGAAT

2801 CACGGAGGCA TCAAGTGACC AACAGGAAA AAACCGCCCT TAACATGGCC CGCTTTATCA GAAGCCAGAC ATTAAACGCTT CTGGAGAAA TCAACGAGCT
GTGCTCCCGT AGTTCACTGG TTTGTCCTTT TTTGGCGGGA ATTGTACCGG GCGAAATAGT CTTCCGTCTG TAATGCGGA GACCTCTTTG AGTTGCTCGA

2901 GGACGCGGAT GAACAGGCAG ACATCTGTGA ATCGCTTCAC GACCACGCTG ATGAGCTTTA CCGCAGGATC CGGAAATGT AAACGTTAAT ATTTGTGTTAA
CCTGCGCCTA CTTGTCCGTC TGTAGACACT TAGCGAAGTG CTGGTGGAC TACTCGAAT GCGCTCTTAG GCCTTTAA TTTGCAATTA TAAAAACAAT

3001 AATTCGCGTT AAATTTTGT TAAATCAGCT CATTTTTTAA CCAATAGGCC GAAATCGCA AAATCCCTTA TAAATCAAAA GAATAGACCG AGATAGGGTT
TTAAGCGCAA TTTAAAAACA ATTTAGTCGA GTAAAAATTT GGTATCCGG CTTTAGCCGT TTTAGGGAAT ATTTAGTTTT CTATCTGGC TCTATCCCAA

3101 GAGTGTGTT CCAGTTTGA ACAAGAGTCC ACTATTAAAG AACGTGGACT CCAACGTCAA AGGCGAAAA ACCGCTATC AGGCTATGG CCCACTACGT
CTCACACAA GGTCAACCT TGTCTCAGG TGATAATTTC TTGCACCTGA GGTGCACTT TCCCGCTTTT TGCGAGATAG TCCGATACC GGTGATGCA

FIG._32D

3201 GAACCATCAC CCTAATCAAG TTTTTCGGG TCAGGTGCC GTAAGCACT AAATCGGAAC CCTAAAGGA GCCCCCGATT TAGAGTTGA CGGGAAAGC
CTTGGTAGTG GGATTAGTTC AAAAAACCC AGCTCCACGG CATTCGTGA TTAGCCTTG GGATTCCCT CGGGGGCTAA ATCTCGAACT GCCCCTTTCG

3301 CGGCGAACGT GGCAGAGAAAG GAAGGGAAGA AAGCGAAGG AGGGCGCTG CAAGTGTAGC GGTACGCTG CGGTAAACCA CCACACCCGC
GCCGCTTGCA CCGCTCTTTC CTTCCTCTCT TTCCCTTTCC TCGCCGCGA TCOCGCGACC GTTCACATCG CCAGTGCAC GCGCATTGGT GGTGTGGGCG

3401 CGCGCTTAAT GCGCCGCTAC AGGGCGCTC CGGATCTGC CTCCGCGCTT TCGGTGATGA CGGTGA AAC CTCTGACACA TGCAGTCCC GGAGACGGTC
GCCGGAATTA CGCGCGATG TCCCGCGGATG GCCTAGGACG GAGCGGCAA AGCCACTACT GCCACTTTG GAGACTGTGT ACGTCGAGG CCCTGCCAG

3501 ACAGCTTGTG TGTAAGCGA TGCCGGGAGC AGACAGCCCC GTCAGGCGGT GTTGGCGGT GTCGGGGCGC AGCCATGACC CAGTCACGTA
TGTCGAACAG ACATTCGCCCT ACGGCCCTCG TCTGTTCCGG CAGTCCGCCA CAACGCCCA CAGCCCCGG TCGGTACTGG GTCAGTGCA

3601 GCGATAGCG AGTGATATCT GGCTTAAC TA GCGGATCA GAGCAGATTG TACTGAGAGT GCACCATATG CCGTGTGAAA TACCGACAG ATGCGTAAGG
CGCTATCGCC TCACATATGA CCGAATTGAT ACGCCGTAGT CTCGTCTAAC ATGACTCTCA CGTGGTATAC GCCACACTTT ATGGCGTGT TACGCATTCC

3701 AGAAAATACC GCATCAGGCG CTCTTCCGT TCCTCGTCA CTGACTCGT GCGCTCGTC GTTCGGCTG GCGAGCGGT ATCAGCTCAC TCAAGCGCG
TCTTTTATGG CGTAGTCCG GAGAAGCGA AGGAGCGAGT GACTGAGCGA CCGGAGCCAG CAAGCCGACG CCGCTCGCA TAGTCAGTG AGTTTCCGCC

3801 TAATACGGT ATCCACAGAA TCAGGGGATA ACGCAGGATA GAACATGTA GCAAAAGCC AGCAACCGT AAAAAGCCG CGTTGCTGGC
ATTATGCCAA TAGGTGTCTT AGTCCCTAT AGTCCCTAT TGCGTCTCTT CTGTGACTCT CCGTTTCCG TCGTTTCCG GTCTTGGCA TTTTTCGGC GCAACGACCG

3901 GTTTTTCAT AGGCTCCGCC CCCCTGACGA GCATCAAAA AATCAGCGT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATA CCAGCGTGT
CAAAAAGTA TCCGAGGCG GGGACTGCT CGTAGTGT TTAGTGCGA GTTCAGTCTC CACCGCTTG GGTGTCTG ATATTCTAT GGTCCGAAA

4001 CCCCCGGAA GCTCCCTCGT GCGCTCTCT GTTCCGACCC TGCCGCTTAC CGGATACCTG TCCCTTCGG TCCCTTCGG AAGCTGGCG CTTTCTCATA
GGGGACCTT CGAGGGAGCA CGCGAGAGA CAAGGTGGG ACGGCAATG GCCTATGGAC AGGCGAAG AGGAAAGCC TCCGACCCG GAAAGATAT

4101 GGTACGCTG TAGGTATCT AGTTCGTGT AGTTCGTGT CTCGAAGCTG GGTGTGTG CCGAACCC CGTTCAGCC GACCGTGG CCTTATCCG
CGAGTGCAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGGTTCGAC CCGACACAG TCGTTGGGG GCAAGTCCG CTGGCGACG GGAATAGGCC

4201 TAACTATCGT CTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAG ATTAGCAGAG CGAGGTATGT AGGCGGTGT
ATTGATAGCA GAACTCAGGT TGGGCCATT TGTGCTGAT AGCGGTGACC GTGCTCGGT ACCATTGTCC TAATCGTCTC GCTCCATACA TCCGCCACGA

FIG._32E

4301 ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT ATTGGGTATC TGGGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG
 TGTCTCAAGA ACTTCACCAC CGGATTGATG CCGATGTGAT CTTCCTGTCA TAAACCATAG ACGGAGACG ACTTCGGTCA ATGGAAGCCT TTTTCTCAAC

 4401 GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTGAAGC ACCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC
 CATCGAGAAC TAGGCCGTTT GTTTGGTGGC GACCATCGCC ACCAAAAAAA CAAACGTTCC TCGTCTAATG CCGGTCTTTT TTTCCTAGAG TTCTTCTAGG

 4501 TTTGATCTTT TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCAATGAG TTATCAAAAA GGATCTTCAC CTAGATCCTT
 AAACAGAAA AGATGCCCCA GACTGCGAGT CACCTTGCTT TTGAGTGCAA TTCCCTAAAA CCAGTACTCT AATAGTTTTT CCTAGAACTG GATCTAGGAA

 4601 TTAAATTTAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGACTAAAC TTGGTCTGAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA
 AATTAAATTT TTACTTTCAA AATTAGTTAG ATTTTCATATA TACTCATTTG AACAGACTG TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT

 4701 TCTGTCTATT TCGTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGSC CCCAGTCTG CAATGATACC
 AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGCA GCACATCTAT TGATGCTATG CCTCCCGAA TGGTAGACCG GGTCCAGCAC GTTACTATGG

 4801 GCGAGACCCA CGCTCACCGG CTCCAGATTT ATCAGCAATA AACAGGCCAG CCGGAAGGC CGAGCGCAGA AGTGGTCCCTG CAACTTTATC CGCCTCCATC
 CGCTCTGGGT GCGAGTGGCC GAGGTCTAAA TAGTCGTTAT TTGGTCGGTC GGCTTCCCG GCTCGCTCT TCACCAGGAC GTTGAATAG GCGGAGGTAG

 4901 CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAAGTAGT CGCCAGTTAA TAGTTTGGC AACGTTGTTG CCATTGCTGC AGGCATCTG GTGTCAGGCT
 GTCAGATAAT TAACAACGGC CCTTCGATCT CATTCATCAA GCGGTCAATT ATCAAAACGG TTGCAACAAC GGTAACGAGG TCCGTAGCAC CACAGTCCGA

 5001 CGTCGTTTGG TATGGCTTCA TTCAGTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT GTGCAAAAAA GCGGTAGCT CCTTCGGTCC
 GCAGCAAAAC ATACCGAAGT AAGTCGAGC CAAGGGTTGC TAGTTCCGCT CAATGTACTA GGGGGTACAA CACGTTTTTT CGCCAATCGA GGAAGCCAGG

 5101 TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTATATCA CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTTT
 AGGCTAGCAA CAGTCTTCAT TCAACCGGCG TCACAATAGT GAGTACCAAT ACCGTCGTGA CGTATTAAGA GAATCACAGT ACGGTAGCA TTCTACGAAA

 5201 TCTGTACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG GCGACCCGAGT TGCTCTTGCC CGGCGTCAAC ACGGGATAAT ACCGCGCCAC
 AGACACTGAC CACTCATGAG TTGGTTCACT AAGACTCTTA TCACATACGC CGTGGCTCA ACGAGAACGG GCCGCAGTTG TGCCCTATTA TGGCGCGGTG

FIG._32F

5301 ATAGCAGAAC TTTAAAGTG CTCATCATTTG GAAACGTTT TCCGGGGCGA AAACCTCTCAA GGATCTTACC GCTGTGTAGA TCCAGTTCTGA TGTAAACCCAC
 TATCGTCTTG AAATTTTCAC GAGTACTAAC CTTTGTGCAAG AAGCCCCGGCT TTTGAGAGTTT CCTAGAAATGG CGACAACTCT AGGTCAAGCT ACATTGGGTG
 5401 TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTTACC AGCGTTTCTG GGTGAGCAGA AACAGGAGG CAAAAAGGG AATAAGGGGG
 AGCAGCTGGG TTGACTAGAA GTGCTAGAAA ATGAAAGTGG TCGCAAGAC CCACTCGTTT TTGTCCTTCC GTTTTACGGC GTTTTCTCC TTATTCCCGC
 5501 ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTCAT ATATTGAAG CATTATACAG GGTATTGTCT TCATGAGCGG ATACATATTT GAATGTATTT
 TGTGCCCTTA CAACCTTATGA GTATGAGAAG GAAAAAGTTA TAATAACTTC GTAAATAGTC CCAATAACAG AGTACTCGCC TATGTATATA CTTACATATA
 5601 AGAAAAATAA ACAAAATAGG GTTCCGGCGA CATTTCCTCCG AAAAGTGCCA CCTGACGCTCT AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG
 TCTTTTATTT TGTTTATCCC CAAGGCGCGT GTAAAGGGG TTTTACCGGT GGAATGCAGA TTCCTTTGTA ATAAATAGTAC TGTAAATGGA TATTTTATC
 5701 GCGTATCAG AGGCCCTTTC GTCTTCAATA CAGGTAGACC TTTCCGTAGAG ATGTACAGTG AAATCCCCGA AATTATACAC ATGACTGAAG GAAGGGAGCT
 CGCATAGTGC TCCGGGAAAG CAGAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTAC TTTAGGGGCT TTAATATGTG TACTGACTTC CTTCCCTCGA
 5801 CGTCATTTCC TGCCGGGTTA CGTCACCTAA CATCACTGTT ACTTTAAAA AGTTTCCACT TGACACTTTG ATCCCTGATG GAAAACGCAT AATCTGGGAC
 GCAGTAAGGG ACGGCCCAAT GCAGTGGATT GTAGTGACAA TGAATTTTT TCAAAGGTGA ACTGTGAAAC TAGGGACTAC CTTTGTGCGTA TTAGACCCCTG
 5901 AGTAGAAGG GCTTCATCAT ATCAATGCA ACGTACAAAG AATAGGGCT TCTGACCTGT GAAGCAACAG TCAATGGGCA TTTGTATAAG ACAAACTATC
 TCATCTTTCC CGAAGTAGTA TAGTTTACGT TGCATGTTTC TTTATCCCCA AGACTGGACA CTTCTGTTGT AGTTACCCGT AAACATATTC TGTGTGATAG
 6001 TCACACATCG ACAAAACCAAT ACAATACAGG TAGACCTTTT GTAGAGATGT ACAGTGAAT CCCCAGAAAT ATACACATGA CTGAAGGAAG GGAGCTCGTC
 AGTGTGTAGC TGTTTGGTTA TGTATGTCTC ATCTGGAAG CATCTCTACA TGTCACTTTA GGGGCTTTAA TATGTGTACT GACTTCTTTC CTTCCGAGCAG
 6101 ATTCCCTGCC GGGTTACGTC ACCTAACATC ACTGTACTT TAAAAAGTT TCCACITGAC ACTTTGATCC CTGATGGAAA ACGCATATC TGGACAGTA
 TAAGGGACGG CCCAATGCAG TGGATTGTAG TGACAATGAA ATTTTTCCTCAA AGGTGAACCTG TGAACCTAGG GACTACCTTT TGCCTATTAG ACCCTGTCTAT
 6201 GAAAGGGCTT CATCATATCA AATGCAACGT ACAAGAAAT AGGGCTTCTG ACCTGTGAAG CAACAGTCAA TGGGCATTTG TATAAGACAA ACTATCTCAC
 CTTTCCCGAA GTAGTATAGT TTACGTTGCA TGTCTCTTTA TCCCGAAGAC TGGACACTTC GTTGTCTAGTT ACCCGTAAAC ATATTCTGTT TGTATAGAGTG
 6301 ACATCGACAA ACCAATACAA TCTACAGGTA GACCTTTCTG AGAGATGTAC AGTGAATCC CCGAAATAT ACACATGACT GAAGGAAGG AGCTCGTCTAT
 TGTAGCTGTT TGGTTATGTT AGATGTCCAT CTGGAAGCA TCTCTACATG TCACCTTTAG GCGTTTAAATA TGTGTACTGA CTTTCTTCCC TCGAGCAGTA
 6401 TCCCTGCCGG GTTACGTCAC CTACATCAC TGTACTTTA AAAAGTTTC CACTTGACAC TTTGATCCCT GATGGAAC GCATAATCTG GGACAGTAGA
 AGGACGGCC CAATGCAGTG GATTGTAGTG ACAATGAAT TTTTTCAAAG GTGAACCTGT AAACCTAGGA CTACCTTTTG CGTATTAGAC CCTGTCTATCT
 6501 AAGGGCTTCA TCATATCAA TGCAACGTAC AAGAAATAG GGCTTCTGAC CTGTGAAGCA ACAGTCAATG GGCATTTGTA TAAGACAAAC TATCTCACAC
 TTCCCGAAGT AGTATAGTTT ACGTTGCATG TTTCTTTATC CCGAAGACTG GACACTTCTG TGTCAAGTAC CCGTAAACAT ATTCTGTTTG ATAGAGTGTG
 6601 ATCGACAAAC CAATACAATC
 TAGCTGTTTG GTTATGTTAG

FIG._32G

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1  TTCAGGCTCG CCGGACATTG ATTATTGACT AGTATTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCATATAT GGAGTTCGCG GTTACATAAC
   AAGCTCGAGC GGGCTGTAAC TAATAACTGA TCAATAATTA TCATTAGTTA ATGCCCCAGT AATCAAGTAT CGGSTATATA CCTCAAGGCG CAATGTAATTG

101 TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG ACCTCAATAA TGACCTATGT TCCCATAGTA ACGCCAATAG GGAATTTCCTA
   AATGCCATTT ACCGGCGGGA CCGACTGGCG GGTGCTGGG GCGGGGTAAAC TGCAGTTATT ACTGCATACA AGGGTATCAT TCGGGTTATC CCTGAAAGGT

201 TTGACGTCAA TGGGTGGAGT ATTTACGGTA AACTGCCAC AACTGCCATC TTGGCAGTAC ATCAAGTATA TCAATGCCCA AGTACGCCCC CTATTGACGT CAATGACGGT
   AACTGCAGTT ACCACCTCA TAAATGCCAT TTGACGGGTG AACCGTCAATG TAGTTACAT AGTATACGGT TCATGCGGGG GATAACTGCA GTTACTGCCA

301 AAATGGCCCG CCTGGCATTA TGCCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC
   TTTACCGGGC GGACCGTAAT ACGGTCTATG TACTGGAATA CCTGAAAGG ATGAACGCTC ATGTAGATGC ATATCAGTA GCGATAATGG TACCACCTAGC

401 GGTTTTGGCA GTACATCAAT GGGCGTGGAT ACCGGTTTGA CTCACGGGGA TTTCCAACTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA
   CAAAACCGT CATGTAGTTA CCGCACCTA TCGCCAACT GAGTGCCCCCT AAAGTTTAC AGGTGGGGTA ACTGCAGTTA CCTCAAACA AAACCGTGGT

501 AAATCAACGG GACTTTTCCAA AATGTCGTAA CAATCCGCC CCATTGACGC AAATGGGCGG TAGGCGTATA CGGTGGGAGG TCTATATAAG CAGAGTCTCGT
   TTTAGTTGCC CTGAAAGGTT TTACAGCATT GTTGAAGCGG GGTAAGTGGG TTTACCCGCC ATCCGCACAT GCCACCTCC AGATATATTC GTCTCGAGCA

601 TTAGTGAACC GTCAGATCGC CTGGAGACGC CATCCACGCT GTTTTGACCT CCATAGAAGA CACCGGGACC GATCCAGCCT CCGCGGCGCG GAACGGTGCA
   AATCACCTGG CAGTCTAGCG GACCTCTGCG GTAGGTGCGA CAAACTGGA GGTATCTTCT GTGGCCCTGG CTAGGTGCGA GCGCGCGGCC CTGCCCACGT

701 TTGGAACGGG GATTCGCCGT GCCAAGAGTG AGTAAGTAC CGCTATAGA GTCTATAGGC CCACCCCTTT GGCTTCGTTA GAACGGCGGT ACAATTAATA
   AACCTTGCGC CTAAGGGCA CCGTTCTCAC TGCAATTCATG GCGGATATCT CAGATATCCG GGTGGGGGAA CCGAAGCAAT CTGCGCGCGA TGTAAATTAT

801 CATAACCTTA TGTATCATAC ACATACGATT TAGGTGACAC TATAGAATAA CATCCACTTT GCCTTTCTCT CCACAGGTGT CCACCTCCAG GTCCAACCTGC
   GTATTGGAT ACATAGTATG TGTATGCTAA ATCCACTGTG ATATCTTATT GTAGGTGAAA CCGAAGAGA GGTCTCCACA GTGAGGGTC CAGGTTGACG

901 ACCTCGGTC TATCGATTGA ATTCACCAT GGGATGGTCA TGTATCATCC TTTTCTTACT AGCAACTGCA ACTGAGTAC ATTACAGATAT CCAGATGACC
   TGGAGCCAAG ATAGCTAACT TAAGTGGTA CCTACCAGT ACATAGTAGG AAAAAGATCA TCGTTGACGT TGACCTCATG TAAGTCTATA GGTCTACTGG

1  M G W S C I I L F L V A T A T G V H S D I Q M T
   ^met ^Start VL ^EcorV

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FIG._33A

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1001 CAGTCCCCGA GCTCCCTGTG CGCTCTGTG GCGGATAGG TCACCATCAC CTGCCGTGCC AGTCAGGATG TGTCACACTGC TGTCAGCCTGG TATCAACAGA
    GTACAGGGCT CGAGGACAG GCGGAGACAC CCGCTATCCC AGTGGTAGTG GACGGCACGG TCAGTCCTAC ACAGTGACG ACATCGGACC ATAGTTGTCT
25 Q S P S S L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K
    ^CDR-L1

1101 AACCAAGAAA AGCTCCGAAG CTTCGTGATT ACTCGGCACT CTTCCTCTAC TCTGGACTCC CTTCTCGCTT CTCTGGTAGC GGTTCGGGA CGGATTTTAC
    TTGGTCTCTT TCAGGCTTC GAAGACTAAA TGAGCCGTAG GAAGGAGATG AGACCTCAGG GAAGACGAA GAGACCATCG CCAAGGCCCT GCCTAAAGTG
59 P G K A P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T
    ^CDR-L2

1201 TCTGACCATC AGCAGTCTGC AGCCGGAAGA CTTCGCAACT TATTACTGTC AGCAATCTTA TACTACTCCT CCCACGTTTC GACAGGGTAC CAAGGTGGAG
    AGACTGGTAG TCGTCAGACG TCGGCCTTCT GAAGCGTTGA ATAATGACAG TCGTTAGAAT ATGATGAGGA GGGTGCAAGC CTGTCCCATG GTTCCACCTC
92 L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E
    ^CDR-L3
    ^Kpnl

1301 ATCAACAGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCATCTGA TGAGCACTTG AAATCTGGAA CTGCTTCTGT TGTGTGCCTG CTGAATAACT
    TAGTTTGCTT GACACCGACG TGCTAGACAG AAGTAGAAGG GCGGTAGACT ACTCGTCAAC TTTAGACCTT GACGAAGACA ACACACGGAC GACTTATTGA
125 I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F
    ^start human kappa

1401 TCTATCCCAG AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA TCGGSHAACT CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC
    AGATAGGGTC TCTCCGGTTT CATGTCACCT TCCACCTATT CCGGGAGGTT AGCCCATTGA GGGTCCTCTC ACAGTGTCTC GTCTGTCTGT TCCTGTCTGTG
159 Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T

1501 CTACAGCCTC AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAGTCTA CGCTTCCGAA GTACCCCATC AGGCTCTGAG CTCGCCCGTC
    GATGTCGGAG TCGTCGTGGG ACTGCGACTC GTTTCGTCTG ATGCTCTTTG TGTTCAGAT GCGGAGCTT CAGTGGGTAG TCCCGGACTC GAGCGGGCAG
192 Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V

1601 ACAAGAGCT TCAACAGGGG AGAGTGTTAA GCTTGGCCGC CATGGCCCAA CTGTGTTTATT GCAGCTTATA ATGCTTACAA ATAAAGCAAT AGCATCACAA
    TGTTTCTCGA AGTTGTCCCC TCTCACAATT CGAACCGGCG GTACCGGGTT GAACAATAA CGTCCAATAT TACCAATGTT TATTTCGTTA TCGTAGTGTT
225 T K S F N R G E C O

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FIG._33B

1701 ATTTACAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TGGTTTGTC AACATCATCA ATGTATCTTA TCATGTCTGG ATCGGGAATT AATTCGGCGC
 TAAAGTGT TTTCGTA AAAGTGACG TAAGATCAAC ACCAAACAGG TTTGAGTAGT TACATAGAAT AGTACAGACC TAGCCCTTAA TTAAGCCGCG

 1801 AGCACCATGG CCTCTGAAAG AGGAACCTGG TTAGGTATCT TCTGAGCGG AAAGAACCAG CTCGTGGAATG TGTGTCAAGT AGGTTGTGGA
 TCGTGGTACC GGACTTTATT GGAGACTTTC TCCTTGAACC AATCCATAGA AGACTCCGCC TTTCTTGGTC GACACCTTAC ACACAGTCAA TCCCACACCT
 *change from C to T, kill KpnI site

 1901 AAGTCCCCAG GCTCCCCCAG AGCAGAAAGT ATGCAAGCA TGCATCTCAA TTAGTCAGCA ACCAGTGTG GAAAGTCCCC AGGTCCCCA GCAGGCAGAA
 TTCAGGGGTC CGAGGGGTCG TCCGTCTTCA TACGTTTCGT ACGTAGAGTT AATCAGTCGT TGGTCCACAC CTTTCAGGGG TCCGAGGGGT CGTCCGTCTT

 2001 GTATGCAAG CATGCATCTC AATTAGTCAG CAACCATAGT CCGCCCCCTA ACTCCGCCCA TCCCGCCCT AACTCCGCC AGTTCGCC ATTCTCCGCC
 CATACGTTTC GTACGTAGAG TTAATCAGTC GTTGGTATCA GGGCGGGGT TGAGGCGGG TCAAGGCGGG TTAAGAGGCGG

 2101 CCATGGCTGA CTAAATTTTT TTAATTTATG AGAGGGCGAG GCGGCTCGG CCTCTGAGCT ATTCCAGAAG TAGTCAGGAG GCTTTTGTGG AGGCCTAGGC
 GGTACCGACT GATTAAAAA AATAAATAG TCTCCGGCTC CGCGGAGCC GGAGACTCGA TAAGGTCTTC ATCACTCTC CGAAAAAAC TCCGGATCCG

 2201 TTTTGC AAA AGCTGTTAAC AGCTTGGCAC TGSCCGTCTG TTTACAACGT CGTACTGGG AAAACCTGG CGTTACCCAA CTTAATCGCC TTGCAGCACA
 AAAACGTTT TCGACAATTG TCGAACCGTG ACGGCAGCA AATGTTGCA GCACGTAGCC TTTTGGGACC GCAATGGGTT GAATTAGCGG AACGTCGTGT

 2301 TCCCCCCTTC GCCAGTGGC GTAATAGCGA AGAGGCCCGC ACGATCGC CTTCGCCAACA GTTGGCTAGC CTGAATGGCG AATGGCGCCT GATGCGGTAT
 AGGGGGGAAG CGGTCCACCG CATATCGCT TCTCCGGGCG TGGCTAGCG GAAGGTTCT CAACGCATCG GACTTACCG TTACCGCGGA CTACGCCATA

 2401 TTTCTCCTTA CGCATCTGTG CGGTATTTC AACCAGCATAC GTCAAAGCAA CCATAGTAG CGCCCTGTAG CGGCGCATTA AGCGCGCGG GTGTGGTGGT
 AAAGAGGAAT GCGTAGACAC GCCATAAAGT GTGGCGTATG CAGTTTCGTT GGTATCATGC GCGGGACATC GCGCGCTAAT TCGCGCCGCC CACACCACCA

 2501 TACGCGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCGCTCCTT TCGCTTCTCTT CCTTCTCTTT CTGCGCACGT TCGCGCGCTT TCCCCGTCAA
 ATGCGCGTCG CACTGGCGAT GTGAACGGTC GCGGATCGC GGGCGAGGAA AGCGAAGAAA GAGCGGTGCA AGCGGCCGAA AGGGGCAGTT

 2601 GCTCTAATC GGGGGCTCCC TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC AAAAAGCTTG ATTTGGGTGA TGGTTACAGT AGTGGGCCAT
 CGAGATTAG CCCCCGAGG AATCCCAAG GCTAAATCAC GAAATGCCGT GGAGCTGGGG TTTTGTGAAC TAAACCCACT ACCAAGTGA TCACCCGGTA

FIG._33C

2701 CGCCCTGATA GACGGTTTTT CGCCCTTTGA CGTTGGAGTC CACGTTCTTT AATAGTGGAC TCCTGTTCCTCA AACGTGAACA AACTCAACC CTATCTCGG
 GCGGGACTAT CTGCCAAAA GCGGAAACT GCAACCTCAG GTGCAAGAAA TTATCACTG AGAACAGGT TTGACCTTGT TGTGAGTTGG GATAGAGCCC

 2801 CTATTTCTTTT GATTTATAAG GGATTTTGGC GATTTCTGCC TATTTGGTTAA AAAATGACCT GATTTAACAA AAATTTAACG CGAATTTTAA CAAAAATATTA
 GATAAGAAAA CTAAATATTC CCTAAACCG CTAAAGCCGG ATAACCAATT TTTTACICGA CTAAATGT TTTHAAATGCG GCTTAAATTT GTTTATATAAT

 2901 ACGTTTACAA TTTTATGGTG CACTCTCAGT ACAATCTGCT CTGATGCCG ATAGTTAAGC CAATCCGCT ATCGTACGT GACTGGGTCA TGGCTGCGCC
 TGCAATGTT AAAATACCAC GTGAGAGTCA TGTTAGACGA GACTACGGCG TATCAATTCG GTTGAGCGA TAGCGATGCA CTGACCCAGT ACGGACGCGG

 3001 CCGACACCCG CCAACACCCG CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCG TTACAGACAA GCTGTGACCG TCCTCCGGGAG CTGCATGTGT
 GGCTGTGGGC GGTGTGGGC GACTGCGGG GACTGCCCGA ACAGACGAGG GCGTAGGG AATGTCTGTT CGACACTGGC AGAGGCCCTC GACGTACACA

 3101 CAGAGTTTTT CACCGTCATC ACCGAAACG CCGAGGCAGT ATTCTTGAAG ACGAAAGGC CTCGTGATAC GCCTATTTTT ATAGGTTAAT GTCATGATAA
 GTCTCCAAAA GTGGCAGTAG TGGCTTTGG CGCTCCGTCA TAAGAACCTC TGCTTTCCCG GAGCACTATG CGGATAAAAA TATCCAATTA CAGTACTATT

 3201 TAATGGTTTC TTAGACGTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA ACCCTATTT GTTTATTTTT CTAATAACAT TCAAATATGT ATCCGCTCAT
 ATTACCAAG AATCTGCAGT CCACCGTGAA AAGCCCCCTT ACACGCGCCT TGGGGATAAA CAAATAAAAA GATTATGTA AGTTATACA TAGGCGAGTA

 3301 GAGACAATAA CCCTGATAAA TGCTTCAATA ATATTGAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TCGGGCATTT
 CTCCTGTTAT GGGACTATTT ACGAAGTTAT TATACTTTTT TCCTTCTCAT ACTCATAGT TGTAAAGCA CAGCGGGAAT AAGGAAAAA ACGCCGTAAA

 3401 TGCCTTCCTG TTTTGTCTCA CCCAGAAACG CTGGTGAAAG TAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA
 ACGGAAGGAC AAAAACGAGT GGTCTTTTGC GACCACCTTC ATTTCTTACG ACTTCTAGTC AACCCACGTG CTCACCCAAT GTAGCTTGAC CTAGAGTTGT

 3501 GCGGTAAGAT CCTTGAGAGT TTTGCGCCCG AAGAACGTTT TCCAATGATG AGCATTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTGATGACGC
 CGCCATTCTA GGAATCTCA AAAGCGGGGC TTCTTGCAA AGGTTACTAC TCGTGAAAT TTCAAGACGA TACACCGCGC CATAATAGG CACTACTGCG

 3601 CCGGCAAGAG CAATCGGTC GCCCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTACA GAAAGCATC TTACGGATGG CATGACAGTA
 GCGCGTCTC GTTGAGCCAG CCGCGTATGT GATAAGATC TTACTGAACC AACTCATGAG TGGTCAGTGT CTTTTCGTAG AATGCCCTACC GTACTGTCTAT

FIG._33D

3701 AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA CTTACTCTTG ACAAGCATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC
TCTCTTAATA CGTCACGACG GTATTGGTAC TCACTATTGT GACGCCGGTT GAATGAAGAC TGTGTCTAGC CTCCTGGCTT CCTCGATTGG CGAAAAACG

3801 ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAAACGA CGAGCGTGAC ACCACGATGC CAGCAGCAAT
TGTTGTACCC CCTAGTACAT TGAGCGGAAC TAGCAACCCT TGGCCTCGAC TTACTTCGGT ATGTTTGTCT GTCGCACTG TGGTGCTACG GTCGTGCTTA

3901 GGCACAACG TTGCGCAAC TATTAACTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA
CCGTTGTTGC AACCGGTTG ATAAATTGACC GCTTGATGAA TGAGATCGAA GGGCCGTGT TAATTATCTG ACCTACCTCC GCCTATTCA ACGTCTGGT

4001 CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG
GAAGACGCGA GCCGGGAAG CCGACCGACC AAATAACGAC TATTTAGACC TCGGCCACTC GCACCCAGAG CGCCATAGTA ACGTCTGTGAC CCCGTTCTAC

4101 GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA
CATTCGGGAG GGCATAGCAT CAATAGATGT GCTGCCCTC AGTCCGTTGA TACCTACTTG CTTTATCTGT CTAGCGACTC TATCCACGGA GTGACTAATT

4201 GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAACTTCA TTTTAAATTT AAAAGGATCT AGGTGAAGAT CCTTTTGTAT
CGTAACCATT GACAGTCTGG TTCAAAATGAG TATATATGAA ATCTAACTAA ATTTTGAAGT AAAAATTAA TTTTCCTAGA TCCACTTCTA GGAAAACTA

4301 AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAGATCA AAGATCTTC TTGAGATCCT TTTTCTCTGC
TTAGAGTACT GGTTTTAGGG AATTGCATC AAAAGCAAGG TGACTCGCAG TCTGGGGCAT CTTTCTTAGT TTCTAGAAAG AACTCTAGGA AAAAAGACG

4401 GCGTAATCTG CTGTTTCAA ACAAAAAAC CACCGCTACC AGCGGTGGTT TGTTTCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT
CGCATTAGAC GACCAACGTT TGTTTTTTTG GTGGCGATGG TCGCCACCAA ACAACGGCC TAGTTCTCGA TGGTTGAGAA AAAGGCTTCC ATTGACCGAA

4501 CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA
GTCGTCTCGC GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CCGTGGTGAA GTTCTGTAGA CATCGTGGCG GATGTATGGA GCGAGACGAT

4601 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA
TAGGACAATG GTCACCGACG ACGGTCACCG CTATTACGCA CAGAATGGCC CAACCTGAGT TCTGTATCA ATGCGCTATT CCGGTGCGCC AGCCCGACTT

FIG._33E

4701 CCGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCCGAA CTGAGATACC TACAGCGTGA GCATTGAGAA AGGCCACGC TTCCCAGAAG
GCCCCCAAG CACGTGTGC GGTGGAACC TCGCTTGCTG GATGTGGCTT GACTCTATGG ATGTGCACT CGTAACCTTT TCGCGGTGCG AAGGGCTTCC

4801 GAGAAAGCGG GACAGGTATC CCGTAAGCGG CAGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG GGAACGCCCT GGTATCTTTA TAGTCCCTGT
CTCTTTCCGC CTGTCCATAG GCCATTGCGG GTCCCAGCCT TGTCTCTCG CGTGCTCCCT CGAAGGTCCC CCTTTGCGGA CCATAGAAAT ATCAGGACAG

4901 GGGTTTCGCC ACCTCTGACT TGAGCGTCTGA TTTTGTGTAT GCTCGTCTAG GGGCGGAGC CTATGGAATA ACGCCAGCAA CGCGGCCCTT TTACGGTTCC
CCCAAGCGG TGGAGACTGA ACTCGCAGCT AAAACACTA CGAGCAGTCC CCGCGCTCG GATACCTTTT TCGCGTCTGT GCGCCGAAA AATGCCAAGG

5001 TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTCTCTGC GTTATCCCT GATTCTGTGG ATACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG
ACCGGAAAC GACCGAANA CGAGTGTA CAAGAGGAGC CAATAGGGA CTAAGACACC TATTGGCATA ATGGCGAAA CTCACCTCGAC TATGGCGAGC

5101 CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAG AGCGCCCAAT ACGCAACCG CCTCTCCCC CGCGTTGGCC GATTCATTAA
GGCGTCGGCT TGCCTGGCTCG CGTCGCTCAG TCACTCGCTC CTTCGCCCTTC TCGCGGGTTA TCGCTTTGGC GGAGAGGGGC GCGCAACCGG CTAAGTAATT

5201 TCCAGTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGA GTGAGCGGCA CGCAATTAAT GTGAGTTACC TCACTCATTG GGCACCCCG GCTTTACACT
AGGTGACCG TGCTGTCCAA AGGGCTGACC TTTCGCCCGT CACTCGCGGT GCGTTAATTA CACTCAATGG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA

5301 TTATGCTTCC GGCTCGTATG TTGTGTGGA TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATTAA
AATACGAAG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA GTGTGCTCTT TGTGCTACT GTACTAATG CTTAATT

FIG._33F

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1  ATTTCGAGCTC  GCGCGACATT  GATTATTGAC  TAGTTATTAA  TAGTAATCAA  TTACGGGGTC  ATTAGTTTCAT  AGCCCATATA  TGGAGTTCGG  CGTTACATAA
   TAAGTCGAG  CCGGCTGTAA  CTAATAACTG  ATCAATAAAT  ATCATTAGTT  AATGCCCCAG  TAATCAAGTA  TCGGGTATAT  ACCTCAAGGC  GCAATGTATT

101  CTTACGGTAA  ATGGCCCGCC  TGGCTGACCG  CCCAACGACC  CCGGCCCAT  GACGTCAATA  ATGACGTATG  TTCCCATAGT  AACGCCAATA  GGGACTTTCC
   GAATGCCATT  TACCGGGCGG  ACCGACTGGC  GGGTTGCTGG  GGGCGGGTAA  CTGCAGTTAT  TACTGCATAC  AAGGGTATCA  TTGCGGTTAT  CCCTGAAAGG

201  ATTACAGTCA  ATGGGTGGAG  TATTTACGGT  AAACCTGCCA  CTTGGCAGTA  CATCAAGTGT  ATCATATGCC  AAGTAGCACC  CCTATTGACG  TCAATGACGG
   TAACTGCAGT  TACCCACCTC  ATAAATGCCA  TTTGACGGGT  GAACCGTCAT  GTAGTTCACA  TAGTATACGG  TTCAATGCGG  GGATAACTGC  AGTTACTGCC

301  TAAATGGCCC  GCCTGGCATT  ATGCCCAGTA  CATGACCTTA  TGGGACTTTC  CTACTTGGCA  GTATATAGTCA  TCGCTATTAC  CATGGTGATG
   ATTTACCGGG  CCGACCGTAA  TACGGGTCA  GTACTGGAAT  ACCCTGGAAG  GATGAACCGT  CATGTAGATG  CATAATCAGT  AGCGATAATG  GTACCACTAC

401  CGGTTTGGC  AGTACATCAA  TGGGCGTGG  TAGCGGTTTG  ACTCACGGGG  ATTTCCAAGT  CTCCACCCCA  TTGACGTCAA  TGGGAGTTTG  TTTTGGCACC
   GCCAAACCG  TCATGTAGTT  ACCCGCACCT  ATCGCCCAAC  TGAGTGCCCC  TAAAGTTCA  GAGGTGGGGT  AACTGCAGTT  ACCCTCAAAC  AAAACCGTGG

501  AAAATCAACG  GGACTTTCCA  AAATGTCGTA  ACAACTCCG  CCCATTGACG  CAAATGGGCG  GTAGCGGTGT  ACGGTGGGAG  GTCTATATAA  GCAGAGCTCG
   TTTTAGTTGC  CCGTAAAGGT  TTTACAGCAT  TGTTGAGGCG  GGGTAACTGC  GTTTACCCGC  CATCCGCACA  TGCCACCCTC  CAGATATATT  CGTCTCGAGC

601  TTTTAGTGAAC  CGTCAGATCG  CCTGGAGACG  CCATCCACGC  TGTTTTGACC  TCCATAGAAG  ACACCGGGAC  CGATCCAGCC  TCCGCGGCGC  GGAACGGTGC
   AAATCACTTG  GCAGTCTAGC  GGACCTCTGC  GGTAGGTGG  ACAAACTGG  AGGTATCTTC  TGTGCCCCCTG  GCTAGGTCCG  AGCGCCCGC  CCTTGCCACG

701  ATTGGAACGC  GGATTCCCCG  TGCCAAGAGT  GACGTAAGTA  CCGCCTATAG  AGTCTATAGG  CCCACCCCTT  TGGCTTCGTT  AGAACGCGGC  TACAATTAA
   TAACCTGCG  CCTAAGGGGC  ACGGTTCTCA  CTGCATTCTCA  GCGGATATC  TCAGATATCC  GGGTGGGGGA  ACCGAAGCAA  TCTTGCGCCG  ATGTTAATTA

801  ACAFAACCTT  ATGPATCATA  CACATACGAT  TTAGGTGACA  CTATAGAATA  ACATCCACTT  TGCCTTTCTC  TCACACAGTG  TCCACTCCCA  GGTCCAAC
   TGTATGGAA  TACATAGTAT  GTGTATGCTA  AATCCACTGT  GATATCTTAT  TGTAGGTGAA  ACGGAAAGAG  AGGTGTCCAC  AGGTGAGGGT  CCAGGTTGAC

901  CACCTCGGTT  CTAATCGATT  AATTCCACCA  TGGGATGGTC  ATGTATCATC  CTTTTTCTAG  TAGCAACTGC  AACTGGAGCG  TACGCTGAGG  TTCAGCTGGT
   GTGGAGCCAA  GATAGCTAAC  TTAAGGTGGT  ACCCTACCG  TACATAGTAG  GAAAAGATC  ATCGTTGACG  TTGACCTCGC  ATCGGACTCC  AAGTCGACCA

1  M G W S C I I L F L V A T A T G A Y A E V Q L V
   ^start signal peptide
   ^met
   ^start of heavy chain
   ^BsiWI

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FIG._34A

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1001 GGAGTCTGGC GGTGGCCTGG TGCAGCCAGG GGGCTCACTC CGTTTGTCCT GTGCAGCTTC TGGCTTCACC ATTAGTGGTT CTGGGATACA CTGGGTGCGT
    CCTCAGACCG CCACCGGACC ACGTCGGTCC CCCGAGTGAG GCAAACAGGA CACGTGGAAG ACCGAAGTGG TAATCACCAA GAACCTATGT GACCCACGCA
25  E S G G G L V Q P G G S L R L S C A A S G F T I S G S W I H W V R
    ^CDR-H1

1101 CAGGCCCCCG GTAAGGGCCT GGAATGGGTT SCTTGGATTG CTCCTTATAG CGGGCTACT GACTATGCCG ATAGCGTCAA GGGCCGTTTC ACTATAAGCG
    GTCCGGGGCC CATTCCCGGA CCTTACCCAA CGAACCTAAC GAGGAATATC GCGCGATGA CTGATACGGC TATCGCAGTT CCCGGCAAAG TGATATTCCG
58  Q A P G K G L E W V A W I A P Y S G A T D Y A D S V K G R F T I S A
    ^CDR-H2

1201 CAGACACATC CAAAACACA GCCTACCTAC AAATGAACAG CTTAAGAGCT GAGGACACTG CCGTCTATTA TTCTGCAAGA GAGGGGGGCT TGTACTGGST
    GTCTGTGTAG GTTTTGTGT CCGATGGATG TTTACTTGTG GAATCTCGA CTCCTGTGAC GGCAGATAAT AACACGTTCT CTCCCCCGCA ACATGACCCA
92  D T S K N T A Y L Q M N S L R A E D T A V Y Y C A R E G G L Y W V
    ^CDR-H3

1301 GTTCGACTAC TGGGTCAAG GAACCCCTGGT CACCGTCTCC TCGGCCCTCCA CCAAGGGCCC ATCGTCTTC CCCTGGCAC CCTCTCCAA GAGCACCTCT
    CAAGTGATG ACCCAGTTC CTTGGGACCA GTGGCAGAGG AGCCGGAGGT GGTTCCCGG TAGCCAGAAG GGGACCCGTG GGAGGAGGTT CTCGTGGAGA
125 F D Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T S
    ^Apa1

1401 GGGGGCACAG CGGCCCTGGG CTGCCCTGGT AAGGACTACT TCCCCGAAACC GGTGACGGTG TCGTGGAACT CAGGCGCCCT GACCAGCGGC GTGCACACCT
    CCCCCGTGTC GCGGGGACCC GACGGACCCAG TTCCTGATGA AGGGGCTTGG CCACCTGCCAC AGCACTTGA GTCCGCGGGA CTGGTCGCCG CACGTGTGGA
158 G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G V H T F

1501 TCCCGGCTGT CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGCGTGGTG ACTGTGCCCT CTAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA
    AGGCCCGACA GGATGTCAGG AGTCTGAGA TGAGGGAGTC GTCGCACACAC TGACACGGGA GATCTCGAA CCGTGGGTC TGGATGTAGA CGTTGCACCT
192 P A V L Q S S G L Y S L S S V V T V P S S S L G T Q T Y I C N V N

1601 TCACAAGCCC AGCAACACCA AGGTGGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAC TCACACATGC CCACCGTGCC CAGCACCTGA ACTCCTGGGG
    AGTGTTCCGG TCCTTGTTGGT TCCACCTGTT CTTTCAACTC GGGTTTAGAA CACTGTGTTG AGTGTGTACG GGTGGCACGG GTCGTGGACT TGAGGACCCC
225 H K P S N T K V D K K V E P K S C D K T H T C P P C P A P E L L G

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FIG._34B

1701 GGACCGTCAG TCCTCTCTT CCCCCAAA CCAAGGACA CCTCATGAT CTCCCGGACC CCTGAGTCA CATCGTGGT GTGGACGTG AGCCACGAAG
 CCTGGCAGTC AGAAGAGAA GGGGGGTTTT GGGTTCTGT GGGAGTACTA GAGGGCTGG GGACTCCAGT GTACGCACCA CCACCTGCAC TCGGTGCTTC
 258 G P S V F L F P P K P K D T L M I S R T P E V T C V V V D V S H E D

 1801 ACCCTGAGGT CAAGTTCAAC TGGTACGTGG ACGGCGTGG GGTGCATAT GCCAAGACAA AGCCGCGGA GGACAGTAC AACAGCACGT ACCGGGTGGT
 TGGGACTCCA GTTCAAGTTG ACCATGCACC TGCCGCACCT CCACGTATTA CGGTTCTGTT TCGGCGCCTT CTTGTCATG TTGTCGTGCA TGGCCCCACCA
 292 P E V K F N W Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V

 1901 CAGCGTCTC ACCGTCTCTG ACCAGGACTG GCTGAATGGC AAGGAGTACA AGTGCAAGGT CTCCAACAA GCCCTCCCAG CCCCCATCGA GAAAACCATC
 GTCCGAGGAG TGGCAGGACG TGGTCTCTGAC CGACTTACCG TTCCTCATGT TCACGTTCCA GAGGTGTTTT CGGAGGGTC GGGGGTAGCT CTTTTGGTAG
 325 S V L T V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I

 2001 TCCAAAGCCA AAGGCGAGCC CCGAGAACCA CAGGTGTACA CCTGCCCC ATCCCGGGA GAGATGACCA AGAACCAAGT CAGCCTGACC TGCCTGGTCA
 AGGTTTCGGT TTCCCGTCGG GGTCTTGGT GTCCACATGT GGGACGGGG TAGGGCCCTT CTCTACTGGT TCITGGTCCA GTCCGACTGG ACGGACCAGT
 358 S K A K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K

 2101 AAGGCTCTA TCCAGCGAC ATCGCCGTGG AGTGGGAGAG CAATGGGCG CCGGAGNACA ACTACAAGAC CAGCCCTCCC GTCTGGACT CCGACGGCTC
 TTCCGAAGAT AGGTCTGCTG TAGCGGCACC TCACCTCTC GTTACCCGTC GGCCTCTGT TGATGTTCTG GTGCGGAGG CAGACCTGA GGCTGCCGAG
 392 G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S

 2201 CTCTCTCTC TACAGCAAGC TCACCGTGA CAAGAGCAGG TGGCAGCAGG GGAACGCTT CTCATGCTCC GTGATGCATG AGGCTCTGCA CAACCACTAC
 GAAGAAGGAG ATGTCTGTCG AGTGGCACCT GTTCTCGTCC ACCGTCTGCC CCTTGCAGAA GAGTACGAGG CACTACGTAC TCCGAGACGT GTTGGTGATG
 425 F F L Y S K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y

 2301 ACGCAGAGA GCCTCTCCCT GTCTCCGGGT AAATGAGTGC GACGGCCCTA GAGTCGACCT GCAGAAGCTT GCGCGCCATG GCCCACTTG TTTATTGCAG
 TCGCTCTCT CCGAGAGGGA CAGAGGCCCA TTTACTCAG CTGCCGGAT CTCAGCTGGA CGTCTTCGAA CCGGCGGTAC CCGGTTGAAC AAATAACGTC
 458 T Q K S L S L S P G K O

 2401 CTTATAATGG TTACAATAA AGCAATAGCA TCACAAATTT CACAAATAA GCATTTTTT CACTGCATTC TAGTTGTGGT TTGTCCAAC TCATCAATGT
 GAATATTACC AATGTTTATT TCGTTATCTG AGTGTTTTAA GTGTTTATT CGTAAAAA GTGACGTAAG ATCAACACCA AACAGGTTTG AGTAGTTACA

FIG._34C

2501 ATCTTATCAT GTCTGGATCG ATCGGGAATT AATTGGGGCG AGCACCATGG CCTGAAATAA CCTCTGAAAG AGGAACCTGG TTAGGTACCT TCTGAGGGGG
TAGAATAGTA CAGACCTAGC TAGCCCTTAA TTAAGCCGGG TCGTGGTACC GGACTTTATT GGAGACTTTC TCCTTGAACC AATCCATGGA AGACTCCGCC

2601 AAAGAACCAT CTGTGGAATG TGTGTCAGTT AGGTGTCGGA AAGTCCCCAG GCTCCCCAGC AGCAGAAAGT ATGCAAGCA TGCATCTCAA TTAGTCAGCA
TTTCTTTGGTA GACACCTTAC ACACAGTCAA TCCCACACCT TTCAGGGGTC CGAGGGGTCT TCCGTCTTCA TAGCTTTCGT ACGTAGAGTT AATCAGTCTG

2701 ACCAGGTGTG GAAAGTCCCC AGGTCCCCA GCAGGCAGAA GTATGCAAG CATGCATCTC AATTAGTCAG CAACCATAGT CCCGCCCTA ACTCCGCCCA
TGGTCCACAC CTTTCAGGG TCCGAGGGT CGTCCGTCTT CATACGTTTC GTACGTAGAG TTAATCAGTC GTTGGTATCA GGGCGGGGAT TGAGGCGGCT

2801 TCCCGCCCCCT AACTCCGCC AGTTCGCCCC ATTCTCCGCC CCATGTTTCTT TTAATTATGC AGAGGCCGAG GCCGCCTCGG CCTCTGAGCT
AGGCGGGGA TTGAGGCGG TCAAGGCGG TAAGAGGCGG GGTACCGACT GATTAAAAA AATAAATACG TCTCCGGCTC CGGCGGAGCC GGAGACTCGA

2901 ATTCCAGAAG TAGTGAGGAG GCTTTTTTGG AGGCCTAGGC TTTTGCAGAA AGCTGTAAAC AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTGACTGGG
TAAGTCTTC ATCACTCCTC CGAAAAAAC TCCGGATCCG AAAACGTTT TCGACAATTG TCGAACCGTG ACCGGCAGCA AATGTTGCA GCACTGACCC

3001 AAAACCCCTG CATTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCTTC GCCAGTTGGC GTAATAGCGA AGAGGCCCGC ACCGATCGCC CTTCGCCACA
TTTTTGGGACC GCAATGGGTT GAATTAGCGG AACGTCGTCT AGGGGGGAG CGGTCAACCG CATATCGCT TCTCCGGGCG TGGCTAGCGG GAAGGTTCT

3101 GTTGGGTAGC CTGAATGGCG AATGGCGCCT GATGGGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTC AACCGCATAC GTCAAAGCAA CCATAGTACG
CAACGCATCG GACTTACCGC TTACCGCGGA CTACGCCATA AAAGAGGAAT GCGTAGACAC GCCATAAAGT GTGGCGTATG CAGTTTCGTT GGTATCATGC

3201 CGCCTGTAG CGGCGCATTA AGCGCGGCGG GTGTGGTGGT TACGCGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCCGCTCCTT TCGCTTTCTT
GGGGACATC GCCGCGTAAT TCGGCGCGCC CACACCACCA ATGCGCGCTG CACTGCGGAT GTGAACGGTC GCGGGATCGG GGGCGAGGAA AGCGAAAGAA

3301 CCTTCTCTT CTGCGCACGT TCGCCGGCTT TCCCCGTCAA GCTCTAATC GGGGGTCCC TTTAGGGTTC CGATTATAGT CTTTACGGCA CCTCGACCCC
GGGAAGGAAA GAGCGGTGCA AGCGGCCGAA AGGGCGAGTT CGAGATTAG CCCCCAGGG AATCCCAAG GCTAATCAC GAAATGCCGT GGAGCTGGGG

3401 AAAAAACTTG ATTTGGGTGA TGGTTCACGT AGTGGGCCAT CGCCCTGATA GACGGTTTTT CGCCTTTGA CGTTGGAGTC CAGCTTCTTT AATAGTGGAC
TTTTTTTGAAC TAAACCCACT ACCAAGTGCA TCACCCGGTA GCGGGACTAT CTGCCAAAAA GCGGAAACT GCAACCTCAG GTGCAAGAAA TTATCACCTG

FIG._34D

3501 TCTTGTTCCTCA AACTGGAACA AACTCAACC CTATCTCGGG CTATCTCTTTT GATTATATAAG GGATTTTGCC GATTTGCGCC TATTGGTTAA AAAATGAGCT
 AGAACACAGGT TTGACCTTGT TGTGAGTTGG GATAGAGCCC GATAAGAAAA CTAAATATTC CTAAGACCGG CTAACCAATT TTTTACTCGA

 3601 GATTTAAACAA AAATTTAACG CGAATTTTAA CAAAATATTA AGTTTACAA TTTTATGGTG CACTCTCAGT ACAATCTGCT CTGATGCCGC ATAGTTAAGC
 CTAAATTTGTT TTTAAATGTC GCTTAAATTT GCTTATAAT TGCAAATGTT AAATATCCAC GTGAGAGTCA TGTTAGACGA GACTACGGCG TATCAATTCG

 3701 CAACCTCCGCT ATCGCTACGT GACTGGGTCA TGGTGCGCC CCGACACCCG CCAACACCCG CTGACGGGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC
 GTTGAGGGCA TAGCGATGCA CTGACCCAGT ACCGACGGG GGTGTGGG GACTGTGGG GACTGTGGG GACTGTGGG ACAGACGAGG GCGTAGGGC

 3801 TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAGGTTTT CACCGTCATC ACCGAAACGC GCGAGGCAGT ATTCTTGAAG ACGAAAGGGC
 AATGTCGTGT CGACACTGGC AGAGGCCCTC GACGTACACA GTCTCCAAA GTGGCAGTAG TGGCTTTGCG CGCTCCGTCA TAAGAACTTC TGCCTTCCCG

 3901 CTCGTGATAC GCCTATTTTT ATAGGTTAAT GTCATGATAA TAATGGTTTC TTAGACGTCA GGTGGCACTT TTCGGGGAAA TGTGGCGGA ACCCCTATTT
 GAGCACATG CGGATAAAAA TATCCAATTA CAGTACTATT ATTACCAAAG AATCTGCAGT CCACCGTGAA AAGCCCTTTT ACACGCGCCT TGGGGATAAA

 4001 GTTTATTTTT CTAAATACAT TCAATATGT ATCCGCTCAT GAGACAATAA CCCTGATAAA TGTCTCAATA ATATTGAAA AGGAAGAGTA TGAGTATTCA
 CAAATAAAAA GATTTATGTA AGTTTATACA TAGCGGAGTA CTCTGTTATT GGGACTATTT ACGAAGTTAT TATAACTTTT TCCTTCTCAT ACTCATAACT

 4101 ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TGCGGCATTT TGCCTTCCTG TTTTGTCTCA CCCAGAAACG CTGGTGAAAG TAAAGATGC TGAAGATCAG
 TGTAAGGCA CAGCGGGAAT AAGGAAAAA ACGCCGTAAA ACGGAAGGAC AAAAAAGAGT GGGTCTTTTC GACCACTTTC ATTTTCTAGC ACTTCTAGTC

 4201 TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCCGCCCG AAGAAGCTTT TCCAAATGATG AGCACTTTTA
 AACCCACGCG CTCACCCAAT GTAGCTTGAC CTAGAGTTGT CGCATTTCTA GGAATCTCA AAGCGGGGC TTCTTGCAA AGGTTACTAC TCGTGAAAT

 4301 AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTGATGACCG CCGGCAAGAG CAACTCGGTC GCGGATFACA CTATTTCTCAG AATGACTTGG TTGAGTACTC
 TTCAAGACGA TACACCCGCG CATATATAGG CACTACTGG GCGGTTCTC GTTGAGCCAG CGCGTATGT GATAAGAGTC TTACTGAACC AACTCATGAG

 4401 ACCAGTCACA GAAAGGATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA CTGGGGCCAA CTTACTTCTG
 TGGTCAGTGT CTTTTCGPAG AATGCCCTACC GTACTGTCTAT TCCTTAATA CGTCACGACG GTATTGGTAC TCACATATGT GACGCGGTT GAATGAAGAC

 4501 ACAACGATCG GAGGACCGAA GGAGCTAACG GCTTTTTTTC ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA
 TGTGTCTAGC CTCCTGGGTT CCTCGATTGG CGAAAAACG TGTGTATCCC CCTAGTACAT TGAGCGGAAC TAGCAACCTT TGGCCTCGAC TTACTTCGGT

FIG. 34E

4601 TACCAACGA CGAGCGTGAC ACCACGATGC CAGCAGCAAT GGCAACAACG TTGGGCAAC TATTAACTGG CGACTACTT ACTCTAGCTT CCCGGCAACA
ATGGTTTGCT GCTCGCACTG TGGTGCTAGG GTCGTCGTTA CCGTTGTTGC AACGCGTTTG ATAATTGACC GCTTGATGAA TGAGATCGAA GGGCCGTTGT

4701 ATTAAPAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGGT CGGCCCTTCC GGCTGCTGG TTTATTGCTG ATAAATCTGG AGCCGGTGAG
TAATTATCTG ACCTACCTCC GCCTATTTC ACGTCTCTGGT GAAGACGGGA GCCGGGAAGG CCGACCGACC AAATAACGAC TATTTAGACC TCGGCCACTC

4801 CGTGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC
GCACCCAGAG CGCCATAGTA ACGTCGTGAC CCCGGTCTAC CATTCGGGAG GGCATAGCAT CAATAGATGT GCTGCCCCCTC AGTCCGTTGA TACCTACTTG

4901 GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA CTGTACAGAC AAGTTTACTC ATATATACTT TAGATTGATT TAAACCTTCA
CTTTATCTGT CTAGCGACTC TATCCACGGA GTGACTAATT CGTAACCAAT GACAGTCTGG TTCAAATGAG TATATATGAA ATCTAACTAA ATTTTGAAGT

5001 TTTTAAATTT AAAAGGATCT AGGTGAAGAT CCTTTTGTAT AATCTCATGA CCAAAATCCC TTATCGTTC ACTGAGCGTC AGACCCCGTA
AAAAATTAAA TTTTCTCTAGA TCCACTTCTA GGAATAACTA TTAGAGTACT GGTTTTAGGG AATTGCATC AAAAGCAAGG TGACTCGCAG TCTGGGGCAT

5101 GAAAAGATCA AAGGATCTT TTTTCTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAC CACCGCTACC AGCGGTGGTT TGTTCGCCGG
CTTTTCTAGT TTCTCTAGAAG AACTCTAGGA AAAAAAGACG CGCATTAGAC GACGAACGTT TGTTTTTTTG GTGCGGATGG TCGCCACCAG ACAAACGGCC

5201 ATCAAGAGCT ACCAATCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACIT
TAGTTCTCGA TGGTTGAGAA AAAGGCTTCC ATGACCCGAA GTCGTCTCG GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CCGTGGTGAA

5301 CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG GTTGGAATCA
GTTCTTGAGA CATCGTGGCG GATGTATGGA GCGAGACGAT TAGGACAAATG GTCACCGACG ACGGTACCG CTATTCAGCA CAGAAATGGCC CAACCTGAGT

5401 AGACGATAGT TACCGGATAA GGGCAGCGG TCGGGCTGAA CGGGGGTTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCCGAA CTGAGATACC
TCTGCTATCA ATGGCTATT CCGGCTGCTT AGCCCGACTT GCGGCTGCGG CACGTGTCTC GGTCTGAACC TCGCTGTCTG GATGTGGCTT GACTCTATGG

5501 TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGG GACAGGTATC CCGTAAACGG CAGGTTCGGA ACAGGAGAGC GCACGAGGGA
ATGTCGCACT CGTAACTCTT TCGCGGTGCG AAGGGCTTCC CTCTTTCCGC CTGTCCATAG GCCATTCGCC GTCCAGCCT TGTCCTCTCG CGTGCTCCCT

5601 GCTTCCAGGG GGAAGGCCT GGTATCTTTA TAGTCTCTG TAGTCTGCTG GGTCTTCCG ACCTCTGACT TGAGGCTCGA TTTTGTGAT GCTGCTCAGG GGGCGGAGC
CGAAGTCCC CCTTTGCGGA CCATAGAAAT ATCAGGACAG CCCAAGCGG TGGAGACTGA ACTCGAGCT AAAAACAATA CGAGCAGTCC CCCCCTCTCG

FIG. _34F

5701 CTATGGAAA ACGCAGCAA CGCGCCCTTT TTACGGTTCC TGGCCTTTGG CTGGCCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCTT GATTCTGTGG
GATACCTTTT TCGCGTTCGT GCGCCGGAAA AATGCCAAGG ACCGGAAC GACCGGAAA CGAGTGTACA AGAAGGACG CAATAGGGA CTAAGACACC

5801 ATAACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG CCGCAGCCGA ACGACCAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAAG AGCGCCCAAT
TATTGGCATA ATGGCGAAA CTCACTCGAC TATGGCGAGC GCGGTGCGGT TGCTGGCTCG CGTCGCTCAG TCACTCGCTC CTTCGCCCTTC TCGCGGGTTA

5901 ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCAATTA TCCAACCTGG ACGACAGCTT TCCCGACTGG AAAGCGGGA GTGAGCGCAA CGCAATTAAT
TGCGTTTGGC GGAGAGGGGC GCGCAACCGG CTAAGTAATT AGTTGACCG TGCTGTCCAA AGGCTGACC TTTCGCCCGT CACTCGCGTT GCGTTAATTA

6001 GTGAGTTACC TCACTCATTG GGCACCCCG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA
CACTCAATGG AGTGAGTAAT CCGTGGGGTC CGAATGTGA AATACGAAG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA GTGTGTCTCTT

6101 ACAGCTATGA CCATGATTAC GAATTA
TGTCGATACT GGTAATAATG CTTAAT

FIG._34G

FIG. 35

Residue	Natural Diversity	Diversity < DNA codon	% good	% covering
L1-28	SNVDGI	SNVDGI<RDT>	100%	94%
L1-29	ISVGN	ISVG<RKT>	100%	86%
L1-29		IV<RTT>	100%	56%
L1-30	SNKGRYTDA	SNKGGRTTDAAE<RVW>	92%	93%
L1-31	SNTRIDKG	SNTTRDKGGAAE<RVW>	75%	95%
L1-31		SNTTRIHK<ANW>	100%	94%
L1-32	YNWFSDR	YNFSDATIV<DHT>	55%	88%
L1-32		YFS<THT>	100%	77%
L2-50	GADWKLES	GAWLSV<KBG>	83%	67%
L2-53	SNTKIR	SNT<AVC>	100%	90%
L3-91	YSRAGH	YSAD<KMT>	75%	74%
		YS<TMT>	100%	66%
L3-92	YGNSDLTHI	YNSDTIFAV<DHT>	67%	64%
		YNSDTA<DMC>	83%	62%
L3-93	SNQTHGDR	SNTGDA<RVT>	83%	80%
		SNTDYAFIV<DHT>	44%	76%
L3-94	STWYLFAPVI	STYLFAPVINDH<NHT>	75%	78%
		STYFIN<WHT>	83%	43%
L3-96	LYWFIRP	LYFPHS<YHT>	67%	52%
		LYFIHN<HWT>	67%	58%
		LFI<HTT>	100%	42%
		LLWR<YKG>	100%	47%
		YF<TWT>	100%	29%

FIG. 36

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Light Chain Designed Diversity
Diversity: $\sim 2.9 \times 10^9$

CDR-L1: diversity $\sim 7 \times 10^3$

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		R	R	V
				Y

CDR-L2: diversity = 18

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

CDR-L3: diversity $\sim 2.3 \times 10^4$

91	92	93	94	96
KMT	DHT	DHT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	F	F	F	L
Y	I	I	H	P
	N	N	I	S
	S	S	L	Y
	T	T	N	
	V	V	P	
	Y	Y	S	
			T	
			V	
			Y	

FIG. 37

Light Chain Designed Diversity
Diversity: $\sim 6.1 \times 10^8$

CDR-L1: diversity $\sim 3.4 \times 10^3$

28	29	30	31	32
RDT	RTT	RVW	ANW	THT
D	I	D	I	F
G	V	E	K	S
I		G	N	Y
N		K	R	
S		N	S	
V		S	T	
		T		
		V		

CDR-L2: diversity = 18

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

CDR-L3: diversity $\sim 1.0 \times 10^4$

91	92	93	94	96
KMT	DMC	RVT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	N	G	F	L
Y	S	N	H	P
	T	S	I	S
	Y	T	L	Y
			N	
			P	
			S	
			T	
			V	
			Y	

FIG. 38

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Light Chain Designed Diversity**CDR-L3: diversity $\sim 1.3 \times 10^3$**

91	92	93	94	96
TMT	DMC	RVT	WHT	HTT
S	A	A	F	F
Y	D	D	I	I
	N	G	N	L
	S	N	S	
	T	S	T	
	Y	T	Y	

FIG. 39**CDR-L1**

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		V	V	V
				Y

CDR-L2

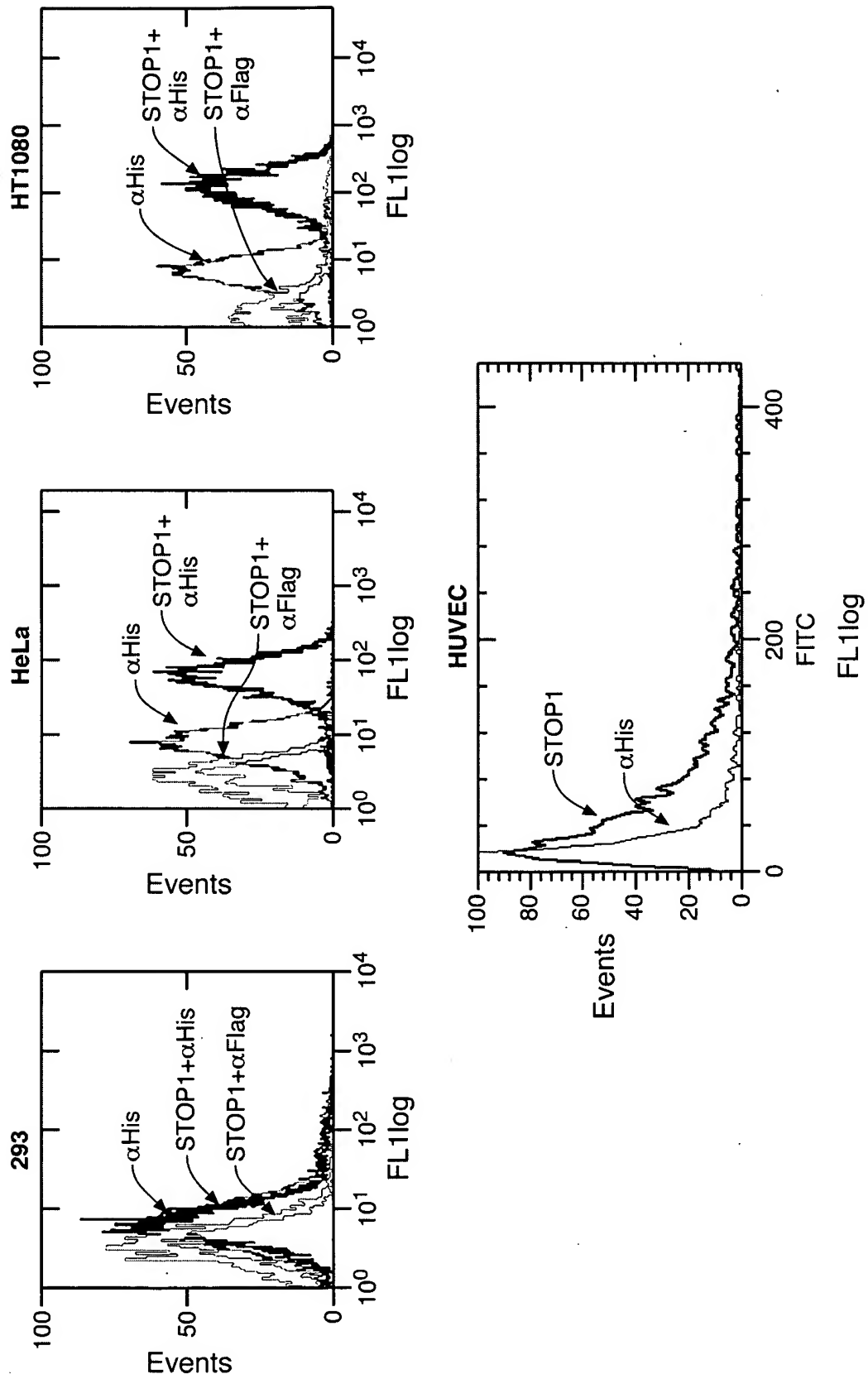
50	53
DVK	AVM
A	N
G	K
L	R
S	S
V	T2
W	

CDR-L3

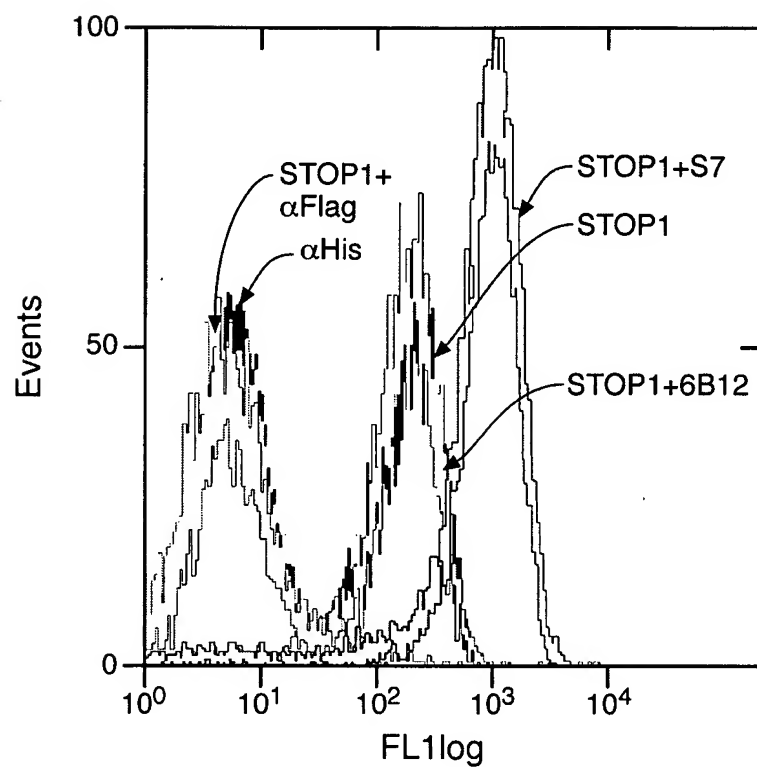
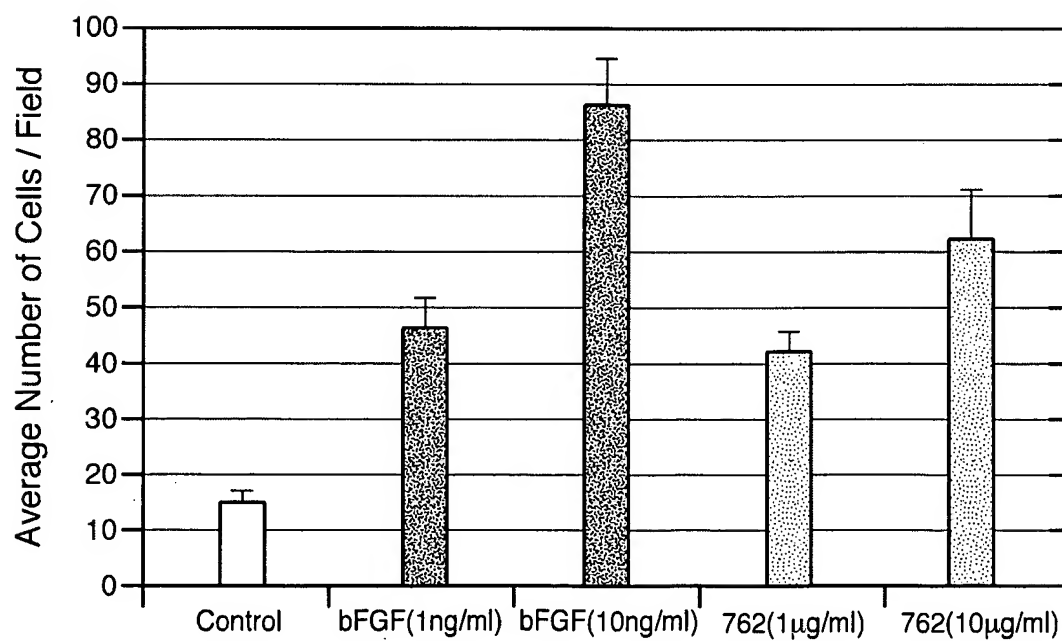
91	92	93	94	96
NRT	NRT	RVM	NNK	TDK
C	C	A2	A	C
D	D	D	C	F
G	G	E	D	L
H	H	G2	E	W
N	N	K	F	Y
R	R	N	G	*
S	S	R	H	
Y	Y	S	I	
		T2	L	
			M	
			N	
			P	
			Q	
			R	
			etc	
			*	

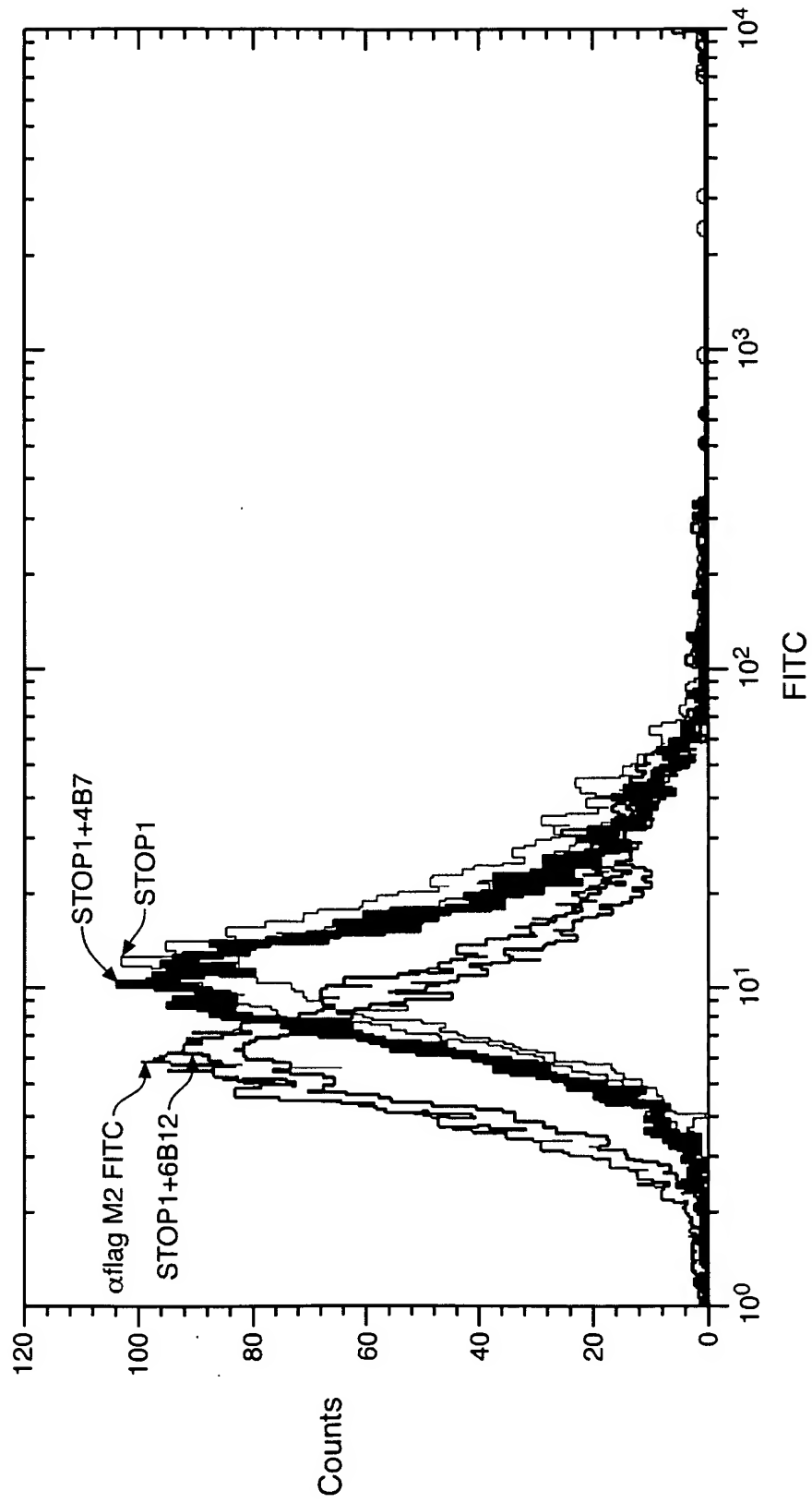
*Amber stop codon is encoded by the degenerate codon

FIG. 40

**FIG. 41**

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**FIG. 42****FIG. 43**

**FIG. 44**

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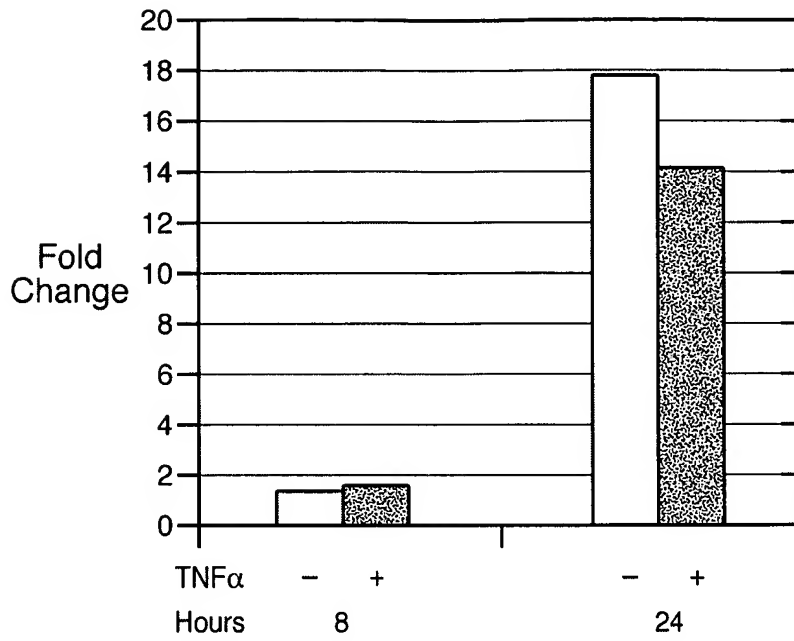


FIG. 45A

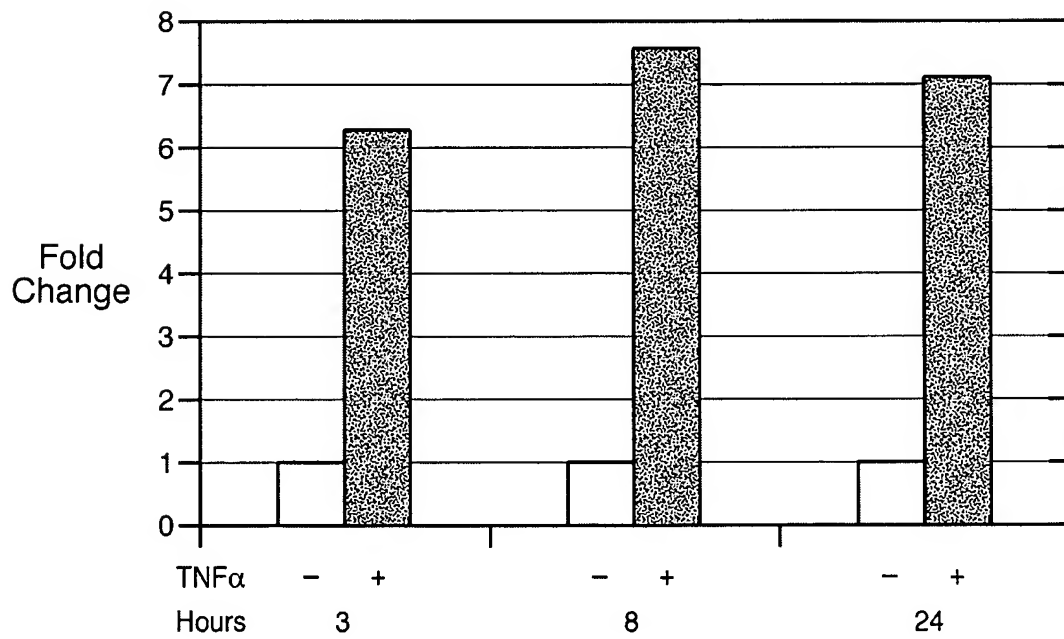


FIG. 45B